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Pred. No. 7.7e-114;
D; Mismatches 234;
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drug abuse, alcoholism, personality traits, compulsive gambling, human immunodeficiency virus dementia, migraine, behaviours in schizophrenic and schizoaffective patients, and suicidal behaviour in patients with schizophrenia. The nucleic acid is useful for detecting the methylation state of all CpG dinucleotides and/or single nucleotide polymorphisms (SNPs). The present sequence is human chemically treated genomic DNA.

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                                                                                                                                                                                                                                                   The invention relates to nucleic acids comprising a segment of chemically pretreated DNA of adrenergic alpha-10-receptor gene. The invention also relates to oligonucleotides or peptide nucleic acid (PNA) oligomers useful for detecting cytosine methylations. The pretreated DNA is useful for the diagnosis or therapy of behavioural disorders, neurological disorders and cancer, in particular major depressive disorder, Tourette's syndrome, schizophrenia, psychiatric and neurological disorders, smoking,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acid useful for diagnosis and therapy of behavioral disorder, neurological disorder and cancer, comprises a sequence of segment of chemically pretreated DNA of adrenergic alpha-1C-receptor gene
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                                                                                                                                                                ACCCCTGAAGATACTGGGACCCGGGCCTTGCCACCCAGTTGGGCTGCCCTTCCCAACTCA
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llarity 76.4%;
Conservative
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Pred. No. 7.7e-114;
O; Mismatches 234;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, ADS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with cytosine methylation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6904 BP; 1244 A; 314 C; 2303 G; 3042 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
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neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
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RESULT 14
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                                                                                                                                                 Human; cytostatic; antidepressant; neuroleptic; nootropic; antiaddictive; adrenergic alpha-1C-receptor; cytosine methylation; therapy; alcoholism; behavioural disorder; neurological; psychiatric; cancer; schizophrenia; Tourette's syndrome; smoking; human immunodeficiency virus dementia;
                             WO200202809-A2
                                                                            Homo sapiens
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Query Match

Similarity

39.6**%**; 70.9**%**;

DB 24;

Length

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Novel nucl disorder,
                                                                                                                             segment
                                                                                                                                                                                               30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                 10-JAN-2002.
                                                                                                                                                                                   (EPIG-)
                                                                                                                            nucleic acid useful for diagnosis and therapy of behavioral der, neurological disorder and cancer, comprises a sequence of and of chemically pretreated DNA of adrenergic alpha-1C-receptor
                                                                                                         1; Page 40-44; 190pp;
                                                                                                                                                                                   EPIGENOMICS
                                                                                                                                                                     Piepenbrock
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2000DE-1043826.
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                                                                                                         English.
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The invention relates to nucleic acids comprising a segment of chemically pretreated DNA of adrenergic alpha-10-receptor gene. The invention also relates to oligonucleotides or peptide nucleic acid (PNA) oligomers useful for detecting cytosine methylations. The pretreated DNA is useful for the diagnosis or therapy of behavioural disorders, neurological disorders and cancer, in particular major depressive disorder, Tourette's syndrome, schizophrenia, psychiatric and neurological disorders, smoking, drug abuse, alcoholism, personality traits, compulsive gambling, human immunodeficiency virus dementia, migraine, behaviours in schizophrenic and schizosffective patients, and suicidal behaviour in patients with schizophrenia. The nucleic acid is useful for detecting the methylation state of all CpG dinucleotides and/or single nucleotide polymorphisms (SNPs). The present sequence is human chemically treated genomic DNA. Sequence 6904 BP; 1244 A; 314 C; 2303 G; 3042 T; 1 other;

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CGCCCCCAGTGCAAGCTCAACCAGGAGGCCTGGTACATCCTGGCCTCCAGCATCGGATCT
                             GTCGTTATTTCGTTGTCGTTTTTTATTTATAAGGGCGATTAGGGGTTTTTAGTCGCGCGGG
                                              GCCGTCATCTCGCTGCCGCCCCTCATCTACAAGGGCGACCAGGGCCCCCAGCCGGGG
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                                                                                       AATTTTAAGCGTATTTCGCGTCGTATTAAGTGTATTATTTTATTGTGTGGTTTATCGTC
                                                                                                                 AACTCCAAGCGCACCCCGCGCCCATCAAGTGCATCATCCTCACTGTGTGGCTCATCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 531.6; DB 2
Pred. No. 1.1e-96;
0; Mismatches 289
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                                                                 17-APR-2000; 2000US-0551744.
10-AUG-2000; 2000US-0636259.
19-OCT-2000; 2000US-0692077.
                                                                                                                                                                                                                                                           WO200179561-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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(LIGG/)
(SMAL/)
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Query Match Best Local S Matches 831

Similarity

34.2%;

Score 459.4; DB Pred. No. 2.1e-82 0; Mismatches 40

.1e-82; 406; 23;

Indels Length

Gaps

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72

189

1383; 78;

1383 BP;

164 A;

482 C; 500 G; 237 T; 0 other;

831;

Conservative

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130

GGCCAGTACTCGGCGGGCGCGGTGGCAGGGCTGGCTGCCGTGGTGGGCTTCCTCATCGTC GACCCCTACTCCGTGCAGGCCACAGCGGCCCATAGGGGGCGGCCATCACCTTCCTCATTCTC

13

73

133 190

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ATCATCCCTTTCTCGCTGGCCAACGAGCTGCTGGGCTACTGGTACTTCCGGCGCACGTGG

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GCGCCACAGAACCTCTTCCTGGTGTCGCTGGCCTCGGCCGACATCCTGGTGGCCACGCTG

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CTGCCGCCCCTCATCTACAAGGGCGACCAGGGCCCCCAGCCGCGCGGGCGCCCCCAGTGC

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The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (I)-(III) by detecting a polymorphic site, comprising; (C) alpha2A or alpha2C or fragment or complement of; and (C) detecting a polymorphic site comprising nucleotide positions 901-909 (I), a site comprising cytosine or guanine at position 753 of (IIV) or altha2B, alpha2C or (III). The method may be used for genotyping an alpha2B, alpha2A or alpha2C receptor gene and further used to determine the position of alpha2B, alpha2A or alpha2A or alpha2C receptor gene and further used to determine which correlate to disease elected from cardiovascular clists of developing a disease comprising site which correlate to disease selected from cardiovascular disease, central nervous system disease and combinations of these. In cardiotine, the technique may be used to predict an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, clonidine, oxymetazoline, guanabenz, UK1304, BHT93 and combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, rauwolscine, idazoxan, tolazoline, phentolamine and combinations of these) by detecting the polymorphic site and correlated to adenylyl cyclase, MAP kinase activity, phosphorylation or inositol phosphate cyclase, MAP kinase activity, phosphorylation or inositol phosphate conscious in the polymorphic site and correlated to adenylyl sequence includes a 12 nucleotide polymorphic site at nucleotides conscious and the alpha-2CAR variant (AAI99933).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting a polymorphic site -
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ALIGNMENTS

## ; CLONE: g178197 US-09-016-434-1181 US-09-016-434-1181 Sequence 1181, Application US/09016434 Patent No. 6500938 GENERAL INFORMATION: APPLICATION NUMBER: US/09/016 FILING DATE: HEREWITH CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE: CLASSIFICATION: APPLICATION NUMBER: FILING DATE: CLASSIFICATION: ATTORNEY/AGENT INFORMATION: NAME: Zeller, Karen J. REGISTRATION NUMBER: 37,071 REFERENCE/DOCKET NUMBER: PA-0 TELECOMMUNICATION INFORMATION: TELEPHONE: (650) 855-0555 TELEPAX: (650) 845-4166 INFORMATION FOR SEQ ID NO: 1181: SEQUENCE CHARACTERISTICS: LENGTH: 2072 base pairs TOPOLOGY: linear IMMEDIATE SOURCE: LIBRARY: GENBANK COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk APPLICANT: Janice Au-Young APPLICANT: Jeffrey J. Seilhamer TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING TITLE OF INVENTION: PATHWAY GENE EXPRESSION NUMBER OF SEQUENCES: 1490 CORRESPONDENCE ADDRESS: TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear STREET: 3174 PORTER DRIVE CITY: PALO ALTO ADDRESSEE: 94304 CALIFORNIA USA INCYTE PHARMACEUTICALS, INC. US/09/016,434 PA-0002

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US-09-016-434-1256
                                                                                                                                              CLONE: 9219405
US-09-016-434-1256
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Patent No. 6500938
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDLUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
COMPUTER: VOICE PC WINDOWS/MS-DOS 6.2
SOFTWARRE: WORD PC-DOS/MS-DOS
COMPATION NOTA:
COURTENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
CLASSIPICATION:
APPLICATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 9A-0002 US
TRIESTNOTOMINICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPHY: (650) 855-0555
                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 1382 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBARK
TYPE: 114645
                               Query Match
Best Local S
Matches 818
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APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
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                               Local Similarity
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                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 845-4166
                                                                  33.1%;
                                         Score 445; DB 4;
Pred. No. 9.7e-80;
0; Mismatches 410
                                                                                                           Length 1382;
                                                            Indels
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                                   GGCGTGGGTGCTATAGGTGGGCAGTGGTGGCGTCGAAGGGCGCAGCTGACCCGGGAGAAG
                                                                                                CAGCAGCCACAGGGCTCCCCGGGTGCTGGCCACCCTACGTGGCCAGGTGCTCCTGGGCAGG
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US-09-016-434-1180
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US-09-016-434-1180
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                                                                  Matches
                                                                                      Best
                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 6500938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1180,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
                                                                                                                                                                                                                                                                 TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 118
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: HEREWIT CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                   IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                    Local
                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                     TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
STREET: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                        LENGTH:
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                     15 CCCCTACTCCGTGCAGGCCACAGCGGCCATAGCGGCGGCCATCACCTTCCTCATTCTCTTT
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                                                                                    Similarity
 GTCTTCAACCAGGATTTCCGGCGATCCTTTAAGCACATCCTCTTCCGACGGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCTTCAACCAGGACTTCCGCCGTGCCTTCCGGAGGATCCTGTGCCGCCCGTGGA 1327
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                                                                  Conservative
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74 PORTER DRIVE
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                                                               Score 432.6; DB 4
Pred. No. 3.1e-77;
0; Mismatches 439
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US-07-676-174A-1
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TELEFAX: (202)822-8944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 3335 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                      Matches
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/676,174A
FILING DATE: 19910328
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WALSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: WT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Eleventh CITY: Washington
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                                                                                                                                                                                                                                          2 TGGACCACCAGGACCCCTACTCCGTGCAGGCCACAGCGGCCATAGCGGCGGCCATCACCT 61
                                                                                                                                                                                                                                                                                                                                      Similarity
TCATTATCGTGCTGACCATCATCGGGAACATCCTGGTGATTCTGAGTGTGTTCACCTACA 730
                                                                                                                                TCCTCATTCTCTTTACCATCTTCGGCAACGCTCTGGTCATCCTGGCTGTGTTGACCAGCC 121
                                                                                                                                                                                        TGGGCCTCCAGCTGGCTGTGCCGGAGTGGGAGGCCCTTCTCACCGCCCTGGTTCTCTCGG
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Eleventh Floor, 1615 L. Street,
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55.9%;
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Octopamine receptor
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Pred. No. 3.7e-28;
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                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,174
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: IBraelsen, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH101.001DV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Venter,
TELEFAX: (6
INFORMATION FOR
SEQUENCE CHARA
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Venter, John C.
APPLICANT: Praser, Claire M.
APPLICANT: McCombie, William R.
TITLE OF INVENTION: OCTOPAMINE RECEPTOR
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,338
FILING DATE: 08-FEB-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, olson
STREET: 620 Newport Center Drive,
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                      STREET: 620 Ne
                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 92660
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             (619) 235-01
OR SEQ ID NO:
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                                                                Patent No. 5760054
GENERAL INFORMATION:
APPLICANT: Thompso
APPLICANT: Huff,
                                                                                                                      Sequence 17,
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Best Local :
             APPLICANT:
TITLE OF IN
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FEATURE:
                                                      APPLICANT:
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HYPOTHETICAL:
                                        APPLICANT:
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LOCATION:
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             NT: Thompson, Wayne J.
NT: Huff, Joel R.
NT: Nerenberg, Jennie I
NT: Lee, Hee-Yoon
NT: Bell, Ian M.
F INVENTION: ALPHALC AL
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SEQUENCES:
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 ALPHAIC ADRENERGIC RECEPTOR ANTAGONISTS 35
                                                                               Wayne J.
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611 TGGGCCTCCAGCTGGCTGTGCCGGAGTGGGAGGCCCTTCTCACCGCCCTGGTTCTCTCGG
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CGCCGCCTAAGGGAGCGAGCCAGGGCCAA 1238
                                               CGCAGCAACCGCAGAGGTCCCAGGGCCAA 629
                                                                                                        TTCTTTATTCCGCTGGCCATCATGACGATCGTCTACATCGAGATCTTCGTGGCCACGCGG
                                                                                                                                                          TTCTTTGCTCCTTGCCTCATCATGATCCTTGTCTACCTGCGCATCTACCTGATCGCCAAA
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Pred. No. 6.4e-24;
0; Mismatches 276;
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; HYPOTHETICAL:
; ANTI-SENSE:
US-08-722-001-17
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Best Local Similarity
Matches 312; Conserv
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229.
FILING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Appollina, Mary A.
REGISTRATION NUMBER: 34,08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (908)594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 921 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/722,001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Rahway
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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CAAGGAGTGCGGGGTCACCGAAGAACCCCTTCTATGCCCCTCTTCTCCTCTCTGGGCTCCTT
                             CCCCCAGTGCAAGCTCAACCAGGAGGCCTGGTACATCCTGGCCTCCAGCATCGGATCTTT 542
                                                                                              CACGCTGGTCACCCGGAGGAAGGCCATCTTGGCCCTGCTCAGTGTCTGGGTCTTGTCCAC 529
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Pred. No. 4.8e-23;
0; Mismatches 229;
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; MOLECULE TYPE:
; HYPOTHETICAL: N
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US-08-722-001-24
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Best Local Similarity
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Patent No. 5760054
                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/229
APPLICATION UNMBER: 1995
ATTORNEY/AGENT INFORMATION:
NAME: Appollina, Mary A.
REGISTRATION NUMBER: 34,08
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                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1567 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US.
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TITLE OF INVENTION: ALPHAIC ADRENERGIC RECEPTOR ANTAGONISTS
NUMBER OF SEQUENCES: 35
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
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Lee, Hee-Yoon
Bell, Ian M.
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57.0%;
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Pred. No. 5.1e-23;
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RESULT 8
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APPLICANT: Jonath
                                               TELEX: (212) 422523 COOP UI INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 376901
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.24 CURRENT APPLICATION DATA:
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LENGTH: 1738 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ZIP: 10112
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E: New York
TRY: U.S.A.
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                                                                                                   (212) 664-0525
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DNA Encoding Human Alpha 1
Receptors and Uses Thereof
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RESULT 9
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HYPOTHETICAL: 1
ANTI-SENSE: N
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LOCATION: 124..16
OTHER INFORMATION:
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Similarity 56.9%;
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Pred. No. 1.1e-22;
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Sequence 3, Application Patent No. 5578611 GENERAL INFORMATION:
APPLICANT: Charles Gluchowski, Carlos C. Forra:
APPLICANT: Theresa A. Branchek, John M. Wetzel
TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC CI
TITLE OF INVENTION: PROSTATIC HYPERPLASIA NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM COMPUTER READABLE FORM: STREET: 30 Rocke CITY: New York STATE: New York COUNTRY: U.S.A. New York 10112 30 Rockefeller Plaza Forray,

ray, George Chiu, el and Paul R. Harti COMPOUNDS TO TREAT

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US-08-228-932-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/228,932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 124..1683
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                     CTACATCCCTCTGGCGGTCATTCTAGTCATGTACTGCCGTGTCTATATAGTGGCCAAGAG
                                                                                 CTTTGCTCCTTGCCTCATCATGATCCTTGTCTACCTGCGCATCTACCTGATCGCCAAACG 602
                                                                                                                    CCCCCAGTGCAAGCTCAACCAGGAGGCCTGGTACATCCTGGCCTCCAGCATCGGATCTTT
                                                                                                                                                                                    CGTCATCTCCATCGGGGCCTCTCCTTGGGTGGAAGGAGCCGGCACCCAA-----CGATGA 698
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(212) 664-0525
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Pred. No. 1.1e-22;
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US-08-468-939-3
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US-08-468-939-3
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APPLICANT: JONATHAN A
TITLE OF INVENTION: D
TITLE OF INVENTION: R
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 311; Conserv
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INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,93
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 124..16
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: sing
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                      GAGCCTGTGCGCCATCTCCATCGATCGCTACATCGGGGTGCGCTACTCTCTGCAGTATCC
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DNA Encoding Human Alpha 1 Adrenergic Receptors and Uses Thereof
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Pred. No. 1.1e-22;
0; Mismatches 230
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RESULT 11
US-08-406-855A-3
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                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/406,855A
FILING DATE: 21-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41337-A-PCT-
TELECOMMUNICATION INFORMATION:
TELEPIAN: (212) 278-0400
TELEPIAN: (212) 278-0400
TELEPIAN: (212) 278-0526
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
 Query Match
Best Local S
Matches 311
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                                                         -08-406-855A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Jonath
                                                                                                                         MOLECULE TYPE: I
HYPOTHETICAL: N
ANTI-SENSE: N
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Jonathan TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1185 Aver
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                   NAME/KEY: CDS
LOCATION: 124..1683
OTHER INFORMATION:
                                                                                                                                                                            LENGTH: 1738 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                 TOPOLOGY:
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1185 Avenue of the Americas
  Conservative
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DNA Encoding Human Alpha 1

Receptors and Uses Thereof
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Score 157; DB 2; Length 1738; Pred. No. 1.1e-22; O; Mismatches 230; Indels
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                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08722190 Patent No. 5990128 GENERAL INFORMATION:
                                                                 COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,190
FILING DATE: 4.APR-1995
CLASSIFICATION: 424
                                                                                                                                                                                                      STREET: LLCK
CITY: New York
TTATE: New York
TT S.A.
                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                             MPUTER TYPE: Flop
                                                                                                                                                                                                                                                               ADDRESSEE:
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ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41878-D-PCT/JPW/AGL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Charles Gluchowski, Carlos C. Forray, George
APPLICANT: Chiu, Theresa A. Branchek, John M. Wetzel and Paul R. Hartig
TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
TITLE OF INVENTION: TREAT BENIGN PROSTATIC HYPERPLASIA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1738 base pair

<u>ω</u>

TELEFAX:

(212) 391-0525

LENGTH: 1738 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: unk MOLECULE TYPE: HYPOTHETICAL: 1

unknown

z

DNA (genomic)

; NAME/KEY: CDS ; LOCATION: 124..16 ; OTHER INFORMATION: US-08-722-190-3

FEATURE: ANTI-SENSE: N

Query Match
Best Local Similarity Matches 311;

Conservative

11.7%;

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Sequence 3, Application US/08244354
PATENT NO. 6015819
GENERAL INFORMATION:
APPLICANT: Charles Gluchowski, et al.
TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS
TITLE OF INVENTION: TREAT BENIEN PROSTATIC HYPERPLASIA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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Pred. No. 1.1e-22;
0; Mismatches 230; Indels
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SEQUENCE CHARACTERISTICS:
LENGTH: 1738 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Sim Matches 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4187
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unkn
MOLECULE TYPE: DI
HYPOTHETICAL: N
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FEATURE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
OF THE PORT OF THE PROPERTY OF THE PROPE
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
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LOCATION: 124..1683
OTHER INFORMATION:
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CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/
FILING DATE: April 1, 1997
CLASSIFICATION: 514
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CAAGGĀGTĠCGGĠGŦĊĀCCGĀAĠĀACĊĊŦTCŦĀTGCĊĊŦCŦŦĊŤĊĊŦCŦCŤĠĠĠĊŤĊCŦŤ
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Pred. No. 1.1e-22;
0; Mismatches 230;
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US-08-244-354-3

COOPER & DUNHAM LLP

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REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAX: (212) 278-0526
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 311; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09206899 Patent No. 683705
GENERAL INFORMATION:
APPLICANT: Jonathan A. Bard et
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1738 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,855
FILING DATE: 21-AUG-1995
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: D
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LOCATION: 124..1683
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
183 GGCCACGCTCATCCATCCTTTCTCGCTGGCCAACGAGCTGCTGGGCTACTGGTACTTCCG
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DNA Encoding Human
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                                                                                                                                                                                             Score 157; DB 3;
Pred. No. 1.1e-22;
0; Mismatches 230
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US-09-444-783-3
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                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1738 base pair
                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4187
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PATENTAL
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/444,78:
FILING DATE:
   MOLECULE TYPE: I
HYPOTHETICAL: N
ANTI-SENSE: N
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                      TOPOLOGY: uni
                                                                                       TYPE: nucleic acid
                                                                                                                                                              TELEX:
                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
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                                                                                                         1738 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Charles Gluchowski, et al.
VENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS
                                                      unknown
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Search completed: February 8, Job time : 95.2013 secs
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; NAME/KEY: CDS;
; LOCATION: 124..1683
; OTHER INFORMATION:
US-09-444-783-3
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                                                                                                                                                                                           543 CTTTGCTCCTTGCCTCATCATGATCCTTGTCTACCTGCCCATCTACCTGATCGCCAAACG 602
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1: /cgn2_6/ptodata/1/pubpna/US07 PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US06 NEW PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06 NEW PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US07 NEW PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07 NEW PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US08 NEW PUB.seq:*

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16: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10N_EW_PUB.seq:*

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18: /cgn2_6/ptodata/1/pubpna/US10N_EW_PUB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US00 NEW_PUB.seq:*
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 15 US-10-001-073-2
9 US-09-825-923-1
15 US-10-077-870-1
15 US-10-077-870-1
15 US-10-071-870-3
15 US-10-071-870-3
15 US-10-305-720-1181
15 US-10-311-455-48
13 US-10-311-455-47
15 US-10-225-567A-43
15 US-10-001-073-40
15 US-10-001-073-25
15 US-10-001-073-25
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Sequence 41, Appl
Sequence 47, Appl
Sequence 47, Appl
Sequence 40, Appl
Sequence 43, Appl
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## ALIGNMENTS

RESULT 1 US-10-001-073-2

Sequence 2, Application US/10001073
publication No. US20030113725A1
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT PILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0

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US-10-001-073-2

Length 1344;

TYPE: DNA ORGANISM: Homo sapiens

SEQ ID NO 2

LENGTH: 1344

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GTTATCTACACCATCTTCAACCAGGACTTCCGCCGTGCCTTCCGGAGGATCCTGTGCCGC
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SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 1344

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1341)
OTHER INFORMATION: Coding sequence for variant human
OTHER INFORMATION: alpha-2B-adrenoceptor protein
US-09-825-923-1
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APPLICANT: Snapir, Amir
APPLICANT: Alhopuro, Pia
APPLICANT: Karvonen, Matti
APPLICANT: Karvonen, Matti
APPLICANT: Koulu, Markku
APPLICANT: Scheinin, Mika
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APPLICANT: Lakka, Timo A
APPLICANT: Lakka, Timo A
APPLICANT: Wyyss"nen, Kristiina
APPLICANT: Myyss"nen, Kristiina
APPLICANT: Kauhanen, Jussi
APPLICANT: Kauhanen, Jussi
APPLICANT: Kauhanen, Jussi
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DORA molecule encoding a variant alpha-2B-adrenoceptor
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
NUMBER OF SRO IN NOS. 10
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GCTTCTGCCAGAGAGGTCAACGGACACTCGAAGTCCACTGGGGAGAAGGAGGAGGAGGAGGAG
                                         CCCCGACCCATGGTGGGGCTTTGGCCTCAGCCAAACTGCCAGCCCTGGCCTCTGTG
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; APPLICANT: Salonen, Jukka T
; TITLE OF INVENTION: Method for detecting a r
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077,870
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: FI 20010323
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 3.1
; SEQ ID NO 1
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1341)
; OTHER INFORMATION: Coding sequence for varius-
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                                                                                                TTCTTTGCTCCTTGCCTCATCATGATCCTTGTCTACCTGCGCATCTACCTGATCGCCAAA
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                                         CGCAGCAACCGCAGAGGTCCCAGGGCCAAGGGGGGGCCTGGGCAGGGTGAGTCCAAGCAG
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300	CURRENT APPLICATION NUMBER: US/10/001,073 ; CURRENT FILING DATE: 2001-11-01 ; NUMBER OF SEQ ID NOS: 53 ; SOFTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 1 ; LENGTH: 1353 ; TYPE: DATE: Homo sapiens ; ORGANISM: Homo sapiens	RESULT 4 US-10-001-073-1 ; Sequence 1, Application US/10001073 ; Publication No. US20030113725A1 ; GENERAL INFORMATION: ; APPLICANT: Liggett, Stephen ; APPLICANT: Small, Kirsten ; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms	Qy 1261 GTTATCTNCACCATCTTCAACCAGGACTTCCGCCGTGCCTTCCGGAGGATCCTGTGCCGC 1320  Db 1261 GTTATCTACACCATCTTCAACCAGGACTTCCGCCGTGCCTTCCGGAGGATCCTGTGCCGC 1320  Qy 1321 CCGTGGACCCAGACGGCCTGGTGA 1344	1141 TGGTTCCCCTTCTTCTTCAGCTACAGCCTGGGCGCCATCTGCCCGAAGCACTGCAAGGTG	1021 CTCCTGGGCAGGGGCTGGGTGCTATAGGTGGGCAGTGGTGGCTCGAAGGGCGCAGCTG	Db 841 ĠĠĊĊĀĠĀĠĠĊĊĀĠĀĀĠĠĀĠĠĠĠĠŤĠŤŦŢĠĠĠĠĠĀŦĊŤĊĊĀĠĀĠĠĀŢĠĀĀĠĠŤĠĀĀĠĠĀĠ 900  Qy 901 ĠĀĠĠĀĠĠĀĠĀĠĀĠĀĠŢĠŢĠĀĀĀĊĊĠĠĀĠŢĠĊĊĀĠĠĀĠĠŢĠĊĊĀĠĠĠĀĠĠŢĠĊ  Db 901 ĠĀĀĠĀĠĀĠĀĠĀĠĀĠŢĠŢĠĀĀĀĊĊĊĠĠĠĊĀĠŢĠĊĊĀĠŢĠĊĊĀĠĠĊŢĊĊĠĠĊĊŢĊĀĠĊŢŢĠĊ 960  901 ĠĀĀĠĀĠĀĠĀĠĀĠĀĠĀĠĀĠŢĠŢĠĀĀĊĊĀĊĀĠĠĊŢĠĊĊĠĠŢĠĊĊĀĊĊŢĀĠĠŢĠĠĊĊĀĠŢĠŢĠĊĊĀĠĠŢĠ  Qy 961 ĀĠĊĊĊĊĊĊĠĊŢĠĊĀĠĠĀĠĊĀĊĀĀĠĠĠŢŢĊĊĊĠĠĠŢĠĊŢĠĊĊĀĊĊŢĀĊĠŢĠĠĊĊĀĠĠŢĠ  Db 961 ĀĠĊĊĊĊĊĠĊŢĠĄĠĊĀĠĊĀĠĊĀĠĠĊŢĊĊĊĠĠĠŢĠŢĠŢĠĊĊĀĠŢĠŢĠĊĊĀĠŢſġ	Db 721 GCTTCTGCCAGAGAGGGTCAACGGACACTCGAAGTCCACTGGGGAGAAGAGAGAG
Qy 1012 GGCCAGGTGCTCGGCCAGGGGCTGGTGCTARAGTGGGCAGTTGGTGGGTGCAAGG 1071	895GAGGAGGAGGAGGAGGAGGAGGAGGACCCCAGGCAGTGTCCCGGCC	Db 721 GCTTCTGCCAGAGAGGTCAACGGACACTCGAAGTCCACTGGGGAGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	Db 601 CCCGACCACGACGAGGGGGCCTAGGGGGGCAGGGCTGGGCCAGGGCCTGGGCCTCGGGGGGGG	OY  481 CHOCCHASTICHANGE CHARACTERS AND CLICAL CONTROL	361 AACTCCAAGCGCACCCGCCGCCGCTCAAGTGCATCCATCC	241 CGGCGCACGTGGTGCGAGGTGTACCTGGCGCTCGACGTGCTCTCTGCACCTCGTCCATC	Qy 121 CGCTCGCTGCGCGCCCTCAGAACCTGTTCCTGGTGTCGCTGGCCGCCGACATCCTG 180

ATGGACCACGAGGACCCCTACTCCGTGCAGGCCACAGCGGCCATAGCGGCCGATCACC 60	; ORGANISM: Homo sapiens ; ORGANISM: Homo sapiens ; FEATURE: ; NAME/KEY: CDS ; LOCATION: (1)(1350) ; OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor ; OTHER INFORMATION: protein US-09-825-923-3  Query Match Best Local Similarity 99.3%; Pred. No. 3.5e-306; Matches 1343; Conservative 0; Mismatches 1; Indels 9; Gaps 1;	S C C O O O O O	APPLICANT: Scholini, Mika APPLICANT: Scholini, Mika APPLICANT: Scholini, Mika APPLICANT: Tuomainen, Tomi-Pekka APPLICANT: Lakka, Timo A APPLICANT: Nyyss"nen, Kristina APPLICANT: Salonen, Ritta APPLICANT: Kauhanen, Jussi APPLICANT: Valkonen, Veli-Pekka TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor TITLE OF INVENTION: protein, and uses thereof	TCAN TCAN TCAN TCAN TCAN	192 201 252 252 261 312 321
Q B Q B Q B Q B Q	2 2 2 2 2 2	5 8 8 8	B & B & B &	\$ \$ \$ \$ \$ \$ \$ \$	00 00 00 00 00 00 00 00 00 00 00 00 00
1072 GCGAGCTGACCCGGGAGAGCGCTTCACCTTCGGCTGGCTG	GECLAGGTEL ACCOUNTE A CONTROL OF THE PROCESS OF THE OF THE		601 CGCAGCAACCGCAGAGGTCCCAGGGCCAAGGGGGGGGCCTGGGCTGGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	CGCCCCCAGTGCAAGCTCAACCAGGAGGCCTGGTACATCCTGGCCTCCAGCATCGAATCT	241 CGGCGCACGTGGTGCGAGGTGTACCTGGCCGTCGACGTGCTCTTCTGCACCTCGTCCATC 300 301 GTGCACCTGTGCGCCATCAGCCTTGGACCGCGCTGAGGCGCGCGC

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Sequence 3, Application US/10077870
Publication No. US20030003470A1
GENERAL INFORMATION:
APPLICANT: Salonen, Jukka T
ITILE OF INVENTION: Method for detecting a ris
FILE REFERENCE: 0933-0.1839
CURRENT APPLICATION NUMBER: US/10/077,870
PRIOR APPLICATION NUMBER: E1 2001-05-21
PRIOR APPLICATION NUMBER: F1 20010323
NUMBER OF SEQ ID NOS: 10
SOSTWARE: Patentin Ver. 3.1
LENGTH: 1353
TYPE: DNA
ORGANISM: Homo sapiens
PEATURE: NAME / NOW.
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; NAME/KRY: CDS
; LOCATION: (1)..(1350)
; OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor protein US-10-077-870-3
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Best Local Similarity
Matches 1343; Conserv
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US-10-077-870-3
                                                                          601 CGCAGCAACCGCAGAGGTCCCAGGGGCCAAGGGGGGGGCCTGGGCAAGGAGTCAAGCAG
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99.3%; Pred. No. 3.5e
tive 0; Mismatches
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es 1; Indels
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RESULT 7

US-10-305-720-1181

/ Sequence 1181, Application US/10305720

/ Publication No. US20040010136A1

/ CENERAL INFORMATION:

/ PPLICANT: AU-Young, Janice K.; Seilhamer, Jeffrey J.

/ TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression of Signaling Pathway Gene Expression Application NUMBER: US/10/305,720

/ CURRENT FILING DATE: 2002-11-26

/ PRIOR APPLICATION NUMBER: 09/016,434

NUMBER OF SEQ ID NOMBER: 09/016,434

NUMBER OF SEQ ID NOS: 1490

// SEQ ID NO 1181

LENGTH: 2072

TYPE: DNA

CRGANISM: Homo sapiens

// PATURE: NAME/KEY: misc_feature

// OTHER INFORMATION: GenBank ID No. US20040010136A1 g178197

US-10-305-720-1181
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PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOPTWARE: PatentIn version 3.1
SEQ ID NO 41
LENGTH: 3274
TYPE: DNA
ORGANISM: Homo sapiens
US-10-225-567A-41
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US-10-225-567A-41
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Publication No. US20030113798A1 
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
                                                                                                                                                                                                                                                                                                                                                                                              98.3%;
Local Similarity 99.2%;
hes 1342; Conservative
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CGGCGCACGTGGTGCGAGGTGTACCTGGCGCTCGACGTGCTCTTCTGCACCTCGTCCATC 300
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Pred. No. 9.3e-306;
0; Mismatches 2;
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Sequence 48, Application US/10311455

Publication No. US20030143606A1

APPLICANT: DEEX, Alexander
APPLICANT: DIEK, Alexander
TITLE OF INVENTION: Diagnosis of Diseases
FILE REFERENCE; 5013.1014
CURRENT FILER REFERENCE; 5013.1014
CURRENT FILING DATE: 2002-12-16
FILE REFERENCE; 5013.1014
CURRENT FILING DATE: 2001-07-02
FRIOR APPLICATION NUMBER: US/10/311,455
FRIOR FILING DATE: 2001-07-02
FRIOR APPLICATION NUMBER: DE 10032529.7
FRIOR PELLORIDATE: 2000-06-30
FRIOR FILING DATE: 2000-09-01
FRIOR FILING DATE: 2000-09-01
SEQ ID NO 48
LENGTH: 6904
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
COTHER IMPORMATION: chemically treated genomic DNA (Homo sapiens)
FRIOR INSULANCE
COTHER INFORMATION: n is a or g or c or t
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Best Local Similarity
Matches 758; Conserv
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76.4%;
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Pred. No. 1.1e-137;
0; Mismatches 234;
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RESULT 9

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Query Match  39.6%; Score 531.6; DB 13; Length 6904;  Best Local Similarity 70.9%; Pred. No. 3.5e-117;  Matches 705; Conservative 0; Mismatches 289; Indels 0; Gaps 0;  Qy  1 ATGGACCACCAGGACCCTACTCCGTGCAGGCCACAGGGCCATAGCGGCCATAGCACC 60	; NAME/KEY: unsure ; LOCATION: 6084 ; OTHER INFORMATION: n is a or g or c or t US-10-311-455-47	; ORGANISM: Artificial Sequence ; PEATURE: ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) ; FEATURE:	R OF SEC NO 47 TH: 6904	PRIOR APPLICATION NUMBER: DE 10032529.7 ; PRIOR FILING DATE: 2000-06-30 ; PRIOR APPLICATION NUMBER: DE 10043826.1 ; PRIOR FILING DATE: 2000-09-01	CURRENT APPLICATION NUMBER: US/10/311,455 CURRENT FILING DATE: 2002-12-16 PRIOR APPLICATION NUMBER: PCT/EPO1/07537 PRIOR FILING DATE: 2001-07-02	BERLIN, Kurt NVENTION: Diagn NVENTION: Cyto NVENTION: 1014	$\sim$	RESULT 10 US-10-311-455-47	Oy 961 AGCCCCCGCTGCAGCAGCCACAGGGCTCCCG 992	Oy 901 GAGGAGGAGGAGGAGAGTGTGAACCCCCAGGCAGTGCCAGTGTCTCCGGCCTCAGCTTGC 960	Qy       841 GGCCAGGGCCAGAAGGAGGTGTTTGTGGGGCATCTCCCAGAGGATGAAGCTGAAGAGAGG       900	Qy 781 ACCCCTGAAGATACTGGGACCCGGGCCTTGCCACCCAGTTGGGCTGCCCTTCCCAACTCA 840	OY 721 GCTTCTGCCAGAGAGGTCAACGGACACTCGAAGTCCACTGGGGAGAGGAGGAGGAGGGGGAG 780	OY 661 CCCCGACCCGACCATGGTGGGGCTTTGGCCTCAGCCAAACTGCCAGCCCTGGCCTCTGTG 720	Oy       601       CGCAGCAACCGCAGAGGTCCCAGGGCCAAGGGGGCCTGGGCAGGGTGAGTCCAAGCAG       660	Db 1364 TTCTTTACTCCTTACCTCATCATAATCCTTATCTACCTACGCATCTACCTAATCGCCAAA 1305
RESULT 11 US-10-001 ; Sequence ; Publical ; GENERAL ; APPLIC ; APPLIC ; APPLIC ; TITLE ; FILE RI ; FUREN	B 8	Qy Db	B 8	B 6	B 8	g Q	B 8	B 6	B Q	B &	B 8	B 8	D Qy	Qy db	ОУ	DЬ
SULT 11 -10-001-073-40 Sequence 40, Application US/10001073 Publication No. US20030113725A1 GENERAL INFORMATION: APPLICANT: Liggett, Stephen APPLICANT: Small, Kirsten TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms FILE REFERENCE: 13073-PCT CURRENT APPLICATION NUMBER: US/10/001,073	961 AGCCCCCGCTGCAGCAGCCACAGGCCTCCCCGG 994	901 GAGGAGGAGGAAGATGTGAACCCCAGGCAGTGCCAGTGTCTCCGGCCTCAGCTTGC 960	841 GGCCAGGGCCAGAAGGAGGGTGTTTGTGGGGCATCTCCAGAGGATGAAGCTGAAGAGGAG 900 	781 ACCCCTGAAGATACTGGGACCCGGGCCTTGCCACCCAGTTGGGCTGCCCTTCCCAACTCA 840	721 GCTTCTGCCAGAGAGGTCAACGGACACTCGAAGTCCACTGGGGAGAAGGAGGAGGAGGGGGAG 780 	661 CCCCGACCCGACGATGGGGGGCTTTGGCCTCAGCCAAACTGCCCAGCCCTGGCCTCTGTG 720	601 CGCAGCAACCGCAGAGGTCCCAGGGGCCAAGGGGGGGCCTGGGCAGGGTGAGTCCAAGCAG 660	541 TICTTIGCTCCITGCCICATCAIGATCCITGTCTACCTGCGCATCTACCTGATCGCCAAA 600	481 CGCCCCAGTGCAAGCTCAACCAGGAGGCCTGGTACATCCTGGCCTCCAGCATCGGATCT 540	421 GCCGTCATCTCGCTGCCGCCCCCTCATCTACAAGGGCGACCAGGGCCCCCAGGCCGCGGG 480	361 AACTCCAAGCGCACCCCGCGCGCATCAAGTGCATCATCCTCACTGTGTGGCTCATCGCC 420	301 GTGCACCTGTGCGCCATCAGCCTGGACCGCTACTGGGCCGTGAGCCGCCGCGCGCG	241 CGGCGCACGTGGTGCGAGGTGTACCTGGCGCTCGACGTGCTCTTCTGCACCTCGTCCATC 300	181 GTGGCCACGCTCATCATCCCTTTCTCGCCTGGCCAACGAGCTGCTGGGCCTACTGGTACTTC 240	121 CGCTCGCTGCGCGCCCCTCAGAACCTGTTCCTGGTGTCGCTGGCCGCCGCCGACATCCTG 180	5061 TTTTTTATTTTTTTTATTATTTTCGGTAACGTTTTGGTTATTTTGGTTGTTTGATTAGT 5120

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; LENGTH: 1386
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-001-073-40
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Best Local Similarity 62.9%;
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NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver.
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Pred. No. 3.6e-101;
0; Mismatches 413; Indels 75;
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Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: LifeSpan Biosciences
APPLICANT: Burmer, Glenna C.
APPLICANT: Burmer, Glenna C.
APPLICANT: Burmer, Glenna C.
FILE REFERENCE: 1920-4-4
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
SOFTWARE: Patentin version 3.1
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LENGTH: 2826
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APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor pol
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 42
LENGTH: 1374
TYPE: DNA
ORGANISM: Homo sapiens
US-10-001-073-42
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Best Local
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       GAGGTCAACGGACACTCGAAGTCCACTGGGGAGAAGGAGGAGGGGGAGACCCCTGAAGAT 792
                                           GÁCGGTGCGTCCCCGACTACCGAAAAACGGGCTGGGCGCGGCGGCAGGCGCAGGCGAGAAC
                                                                                CATGGTGGGGCTTTGGCCTCAGCCAAACTGCCAGCCCTGGCCTCTGTGGCTTCTGCCAGA
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                                                                                                                      -CGCTCAGCGAGAAGCGCGCCCCCGTGGGCCCC
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WESULT 14 US_1001073 Sequence 25, Application US/10001073 Sequence 25, Application US/10001073 Sequence 25, Application US/2000113725A1 Publication No. US20030113725A1 Publication No. Sequence 13073-Ecc PILE REFERENCE: 13073-Ecc	Qy  193 ACTROGACCCGGGCCCTTGCCACCCAGTTGGGCTGCCCTTCCCAACTCAAGGCCAGGGCAAGGAAGAAG
Qy  786 TGAMGATTACTGGACCCTIGCTACCTACT Db  858 CGAC	Oy  195 CATCCCTTTCTCGCTGGCCAACGAGCTCATGGGCTACTTGGTACTTCCGGGCGCACGTGGTC 254

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Sequence 39, Application US/1022557A

Publication No. US20030113798A1

GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: ROUSH, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR FILE REFERENCE: 1920-4-4

CURRENT APPLICATION NUMBER: US/10/225,567A

CURRENT APPLICATION NUMBER: 60/257,144

PRIOR APPLICATION UMBER: 60/257,144

PRIOR APPLICATION DATE: 2001-12-19

PRIOR APPLICATION DATE: 2001-12-19

PRIOR APPLICATION DATE: 2001-12-19

NUMBER OF SEQ ID NOS: 2392

CORTANDE, DESCRIPTION STATES

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; ORGANISM: Homo sapiens
US-10-225-567A-39
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Best Local Similarity 62.9%;
Matches 844; Conservative
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                                                                                     TGCTCCTTGCCTCATCATGATCCTTGTCTACCTGCGCATCTACCTGATCGCCAAACGCAG
                                                                                                                            GCGCTGCGAGATCAACGACCAGAAGTGGTACGTCATCTCGTCGTGCATCGGCTCCTTCTT
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Pred. No. 1.2e-96;
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   TGGACCCAGACGGCCTGGTGA 1344
                                                                 ATCTACACCATCTTCAACCAGGACTTCCGCCGTGCCTTCCGGAGGATCCTGTGCCGCCCG 1323
                                                                                                         CGCACGCTCTTCAAATTCTTCTTCTGGTTCGGCTACTGCAACAGCTCGTTGAACCCGGTC 2151
                                                                                                                                 CATGGCCTCTTCCAGTTCTTCTTCTGGATCGGCTACTGCAACAGCTCACTGAACCCCTGTT 1263
                                                                                                                                                                           TICCCCTTCTTCATCTACACGCTCACGGCCGTCGG------GTGCTCCGTGCCA
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                                        ATCTACACCATCTTCAACCACGATTTCCGCCGCGCCTTCAAGAAGATCCTCTGTCGGGGG 2211
                                                                                                                                                                                                       TTCCCCTTCTTCAGCTACAGCCTGGGCGCCATCTGCCCGAAGCACTGCAAGGTGCCC 1203
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Search completed: February 8, 2004, 01:46:28 Job time : 523.283 secs

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10496.265 Million cell updates/sec
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       ECAA2BAR
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AK046802 Mus muscu
                                                                                                                        Description
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AL606560.1 GI:15591917
AL606560.1 GI:15591917
GSS; Alpha2 adrenergic receptor gene.
GSS; Alpha2 adrenergic receptor gene.
Equus caballus (horse)
Equus caballus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
1 (bases 1 to 872)
Hunter, C. and Elgar, G.
Alpha2 adrenergic receptor gene
Unpublished
                                                                                                                             2 (bases 1 to 872)
2 (bases 1 to 872)
4 Uniter, C.
Birect Submission
Submitted (14-SBP-2001) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB. UK Email:
                                                                                                                      biohelp@hgmp.mrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Horse alpha2 adrenergic receptor gene fragment probably subtype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ECAA2BAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic survey sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Equus caballus"
/mol_type="genomic DNA"
/db_xref="taxon:9796"
                                                                                             Cocation/Qualifiers
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AL284651 Tetraodon
AL530417 AL530417
CD360383 AGENCOURT
CD360119 AGENCOURT
AL606568 Sea Horse
CC240340 CH261-121
AL217170 Tetraodon
CD360520 AGENCOURT
AL174113 Tetraodon

GSS 14-SEP-2001

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AL606539 Chameleon AL606561 Lamprey a AL588968 AL588968 T39448 ya06a09.r2 AL606576 Sturgeon AL60654 Ostrich a BU377890 603588616

BU376517 603807849

AW785035 115829 MA AL237702 Tetraodon AL606541 Chicken a CD361190 AGENCOURT AL573897 AL573897 AL606580 Toothcarp AL549866 AL549866

AW916723 EST348027 AL544577 AL544577

AL544609 AL544609
AL530418 AL530418
AD681729 AGENCOURT
BB643669 BB643669
AK046211 Mus muscu
CA477609 AGENCOURT
BZ138792 CT230-256
AL236849 Tetraodon
BU468891 603365259
CD552619 B0346C06AL606540 Chicken a
AL205895 Tetraodon
BI459381 6033200147

Matches

COUNT

156

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Query Match
Best Local
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AGENCOURT 8113358 Lupski_dorsal_root_ganglion
clone IMAGE:6179035 5', mRNA sequence.
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Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. James R. Lupski

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM13559 row: 1 column: 20

High mnality Regmence ston. 420
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1 (bases 1 to 1044)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6179035"
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/dev stage="adult, 36 yr"
/lab_host="DHIOB"
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0; Mismatches 23;
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RESULT 2
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                                                                                                                                                                                                                        through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 73 Row: o Column: 16
This clone was selected for flowing sequencing because it
passed the following selection criteria: matched mRNA gi: 15718669
This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) &
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anu
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens, (IMAGE:5266354,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
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Mammalia; Eutheria; Primatee; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                         distribution: MGC clone distribution information can
                               /tissue_type="Testis"
/clone_Tib="NIH_MGC_97"
/lab_host="DH10B"
/note="Vector: pBluescript"
/note="Vector 721 g 470 t
                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5266354"
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                                     GGCGCGGGCCGGGGGCGACGGGGATCGGG----
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62.9%;
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Pred. No. 1.6e-77;
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                                         Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishi, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Alzawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuchi D., Kuchi D., Kuchi D., Kuchiwa, H., Kuchi D., Kuchi D., Kuchiwa, H., Kuchi D., Kuchi D.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
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Mus musculus 10 days neonate medulla oblongata cDNA, RIKEN
full-length enriched library, clone:B830011M21 product:ALPHA-2A
ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR), full
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Mammalia; Eutheria; Rodentia;
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Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                      Fukuda, S.,
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Physical and Chemical Research (RIKEN), Laboratory for Genome Riken Yokohama Institute; 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama Institute; 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Fax:81-45-503-9216;

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to
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Please visit our web site for further details.
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The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Carninci, P.,

INOTE="ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR) (SWISSPROT Q01338, PASTY, 99.6%ID, 100%length, match=1351) 'tissue type="medulla oblongata"
(clone Tib="RIKEN full-length enriched
dev\_stage="10 days neonate" /mol\_type="mRNA" /strain="C5PL/6J" /db\_xref="FANTOM\_DBLB830011M21" /db\_xref="taxon:T0090" mouse cDNA library"

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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5594.f For
more information about this cluster, see
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1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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 TACTCCGTGCAGGCCACAGCGGCCATAGCGGCCGCCATCACCTTCCTCATTCTCTTTACC
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                                                                                                                            155
                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                    24.1%;
74.8%;
                                     0;
                                   Score 324; DB 9;
Pred. No. 1.1e-53;
0; Mismatches 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                  Length 1201;
                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                              On Feb 13, 2001 this sequence version replaced gi:12793911.

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
division of Invitrogen. This sequence belongs to sequence cluster
style for more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSDD007BC010P1&cluster=5594.f. Contact:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODD007BC010P1.
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1 (Dases 1 to 1201)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
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1201 bp mRNA linear EST 23-MAY-2003
AL530418 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
CDNA clone CSODD007YE02 5-PRIME, mRNA sequence.
AL530418
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODD007YE02"
                                                                                                                 tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
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                                                                             RESULT 7
BQ887729
LOCUS
DEFINITION
BQ887729
988 bp mRNA linear EST 16-AUG-2002
AGENCOURT_8764335 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6313133
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FEATURES

Db	Ş	<b>8</b>	γQ	DЬ	Ş	Dъ	Ş	DЪ	Ş	DЪ	Ş	Db	β	DЬ	Ş	дb	Ş	Ф	Ş	日	γQ	DЬ	8	ф	γQ	Db	Ş	Que Bes Mat	BASE C
1161 GCGCAAATGCYCBAWKGGGYYYCCMTTTYRAACCA 1195	- 2	1101 CGTGAGCGGACRAAACMGCGGGGGGGGGGGGGGGGGGGGGGGG	723 TTCTGCCAGAGAGGTCAACGGACACTTCGAAGTCCACCCCCCCC	1041 CGAAAARGGCTGGGCGCGGGGAGGGCGAGGCGAAAAMCGGCCTCTGTGGC 722			603 CAGCAACCGCAGAGGTCCCAAGGGCCAAGGGCCAAGGGCCAAGCT 980	921 CTTCGCGCCCTGCCTCAACAWGGGCCTTGTCTACGCGCATCTCCCCTAACG 602	543 CTTTGCTCCTTGCCTCATCATGATCCTTGTCTACCTCCATCATCTACCTCCATCATCATCATCATCATC		483 CCCCCAGTGCAAGCTCAAACCTCAACCCCCCCCCCCCCC	:	423 CGTCATCTCGCTGCCGCCCCTCATCTACAACCCCCCCCCC	744 CCTGAAGCGCACACCACGCGCGTCAAGGCTCATCATCATTCGCCGCGC 422	363 CTCCAAGCGCACCCCGCGCCATCAAGTGCATCATCATCATCATCATCATCATCATCATCATCATCATC	684 GCATCTGTGTKCCAACAGCCTGGACCGCTACTGKCGCGCGCGCGCGCGCGAGTACAA 362	303 GCACCTGTGCGCCATCAGCCTGGACCGCTACTGGGCCTGCTGGGCCGCTGGATCGT 683	624 GCAGGTGTKGTGCGGCGTGTACCTGGGCGCTCGATCTKCTGTACCTGCATCGTACCTGGACCTGGATCTKCTGTTTTTTCAAACATCTTCTTTTTCAAACATCTTCTTTTTCAAACATCTTCT	243 GCGCACGTGGTGCGAGGTGTACCTGGCGCTCCTCCACCTCCTTCTTCCGCGCTACTTCCGG 623	564 GGCCACGCTGGTCATGCCCTTCGTTGGCCAACGACGTACTGCGTACTTCCG 242	183 GGCCACGCTCATCATCCCTTTCTCGCTGGCTGACCTACCT	505 GGCGCTGCGC-CCCCACAAAACCTCTTCCTGGTGTCCCTGCTTGCCTTGC	123 CTCGCTGCGCGCCCTCAGAACCTGTTCCTGGTTTCCTGGTCTCCCGCCGCCGCGCGGCCGGCGG	445 CCTCATCGTCTTCACCGTTGTGGGCAACGTGCTGCTGATTCACCAGCCG 122	63 CCTCATTCTCTTTACCATCTTCGGCAACGCTCTGGTGTGTGT		CCCCTATACCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	ery Match  24.0%; Score 322.4; DB 9; Length 1201; st Local Similarity 60.9%; Pred. No. 2.3e-53; tches 496; Conservative 33; Mismatches 282; Indels 4. Conservative	/clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED" /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR v sites of the pCMVSPORT 6 vector. Library was normalized."  161 a 412 c 389 g 175 t 64 others

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-remail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
CDNA Library Preparation: ResGen, Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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BQ887729
BQ887729.1 GI:222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM13739 row: m column: 06
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
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CTCCAGCATCGGATCTTTCTTTGCTCCTTGCCTCATCATGATCCTTGTCTACCTGCGCAT 584
                                      GCCCGACGGCGCCCTATCCGCAGTGCGGCCTCAACGATGAGACCTGGTACATCTTGTC
                                                                                                                                                  TGTGTGGCTCATCGCCGCCGTCATCTCGCTGCCCCCCTCATCTACAAGGGCGACCAGGG
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                                                                               CCCCCAGCCGCGGGCGCCCCCAGTGCAAGCTCAACCAGGAGGCCTGGTACATCCTGGC
                                                                                                                        CGTGTGGCTCATCTCCGCTGTCATCTCCTTCCCGCCTCTCGTCT----CGTTCTACCGCCG
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/clone="IMAGE:6313133"
/clone=lib="DH10B (phage-resistant)"
/clone lib="NIH MGC 129"
/note="Organ: offactory epithelium; Vector:
/note="Organ: offactory epithelium; Vector:
pcMV-SPORT6.1.ccdb; Site_1: EcoRV; Site_2: Not1; Cloned
unidirectionally. Primer: Oligo dT. Average insert size
unidirectionally. Primer: Oligo dT. Average insert size
2.2 kb. Constructed by Resden, Invitrogen Corp. Note: this
is a NIH_MGC Library."
349 c 300 g 181 t
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|mol_type="mRNA"
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Rodentia;
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RESULT 8
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URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,Y., Tanaka,T., Matsuura
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                                                                                                                                                                                                                                                                                                                                                            Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa K., Bihida S. Hara A Troh M Kawai T chihara V and K. Bihida S. Hara A Troh M Kawai T chihara V and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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quadrigemina Mus musculus cDNA clone B230352011 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                        further details.
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Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                              Computational Analysis of Full-Length Mouse cDNAs Compared with uman Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
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                                                                                                                                                                    organism="Mus musculus"
/mol_type="mRNA"
/tissue_type="corpora quadrigemina"
/dev_stage="adult"
                                                                                                 /db_xref="taxon:10090"
/clone="B230352011"
                                                                      sex="male"
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2736 bp mkNA LINEAL DIC US-DECENTRY
Mus musculus adult male corpora quadrigemina cDNA, RIKEN
full-length enriched library, clone:B230352011 product:unknown EST,
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/clone_lib="RIKEN full-length enriched, adult male
quadrigemina"
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Pred. No. 9.1e-45;
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                            HTC 05-DEC-2002
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Arakawa, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishi, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konmo, H., Adachi, J., Fukuda, S., Arakawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagmer, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shbata, Y., Storch, K., F., Suzuki, H., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., F., Suzuki, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annot, of 60,770 full-length cDNAs

L Nature 420, 563-573 (2002)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria; Rodentia;
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Plate: LLAM14321 row: e column: 02
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Tissue Procurement: Dr. Chi-Bin Chien
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National Institutes of Health, Mammalian Gene Collection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Danio rerio (zebrafish)
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                     CCTCAGAACCTGTTCCTGGTGTCGCTGGCCGCCGACATCCTGGTGGCCACGCTCATC 195
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                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                         /clone="IMAGE:6801483"
/tissue_type="embryo"
/lab_host="DH108 (T1-resistant)"
/clone_lib="NCI CGAP ZEmb3"
/clone_lib="NCI CGAP ZEmb3"
/note="Vector: pCMV-SPORT6.ccdb; Site_1: EcoRV; Site_2:
/noti; Cloned unidirectionally. Primer: Oligo dT. Average
insert size 2.1 kb. Constructed by J. Wang (Research
Genetics, Invitrogen Corp) from tissue donated by L. Zon
(Harvard University). Note: this is a NCI_CGAP Library."
287 c 266 g 200 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
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                                                                                                                                                                                                                                                                                                                                                                                                                  Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
plate: 256 row: D column: 20
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Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Norway rat)
Rattus norvegicus
Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae;
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Tel: 301 838 0200
Fax: 301 838 0208
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Rat BAC End Sequences from Library
Unpublished
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Jong,P. and Fraser,C.M.
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Class: BAC ends.
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                                    /cell_type="Brain"
/clone_lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site_l:
/note30 Rat (BN/S8NH6d/MCW) BAC
Pieter de Jong"
a 200 c 220 g 118 t
                                         ש
                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
                                                                                                                                                                                     /sex="Female"
                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                           clone="CH230-256D20"
                                                                                                                                                                                                                                                                                                    organism="Rattus norvegicus"
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23 CCGTGCAGGCCACAGCGGCCATAGCGGCCGCCCATCACCTTCCTCATTCTCTTTACCATCT
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact freshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                                Estimate of human gene number provided by using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                                                                                                                                                                                                           Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fish Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.
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                                     1 (bases 1 to 736)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.
Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                        Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Archosauria; Gallus.
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: Simon. Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 01612360409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PO Box 88,
                                                                                                                                                             TCTCGCTGCCGCCCTCATCTACAAGGGCGAGCGAGGGCCCCCAGCCGCGCGGGGGGCGCCCCC
                                                                                                                                                                                                                                                                                                            AGCGCACCCCGCGCCGCATCAAGTGCATCATCCTCACTGTGTGGCTCATCGCCGCCGTCA
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                                                                                                       CTCCTTGCCTCATCATGATCCTTGTCTACCTGCGCATCTACCTGATCGCCAAACGCAGCA
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                                 613
 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research (1996): 791, except that a significantly longer reannealing hybridization was used."

214 c 192 g 180 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA was blunted, ligated to Notl adapters, digested with EcoRI size-selected, and cloned into the Notl and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="CSEQRBN21"
/note="Organ: ovary; Vector: pBluescript II KS(+);
/note="Organ: ovary; Vector: pBluescript II KS(+);
ECORI; Site 2: Not1; This normalized library was
constructed from 1 million independent clones. cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="Layer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Gallus gallus"
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71.8%;
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Pred. No. 8.1e-34;
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10b,
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B0346C06-5 NIA Mouse E9.5 Whole Embryo cDNA Library (Long) Mus
ENGRECULUS CDNA clone NIA:B0346C06 IMAGE:30433469 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 570)
Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD552619
CD552619.1 GI:31600350
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Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, U
Email: cdna@lgsun.grc.nia.nih.gov
Plate: B0346 row: C column: 06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    method
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                                  from 6.1 ug of total RNA, treated with T4 DNA polymerase, from 6.1 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by phenol/chloroform, and separated from free linkers by centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were by phenol/chloroform and NotI enzymes and cloned into digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. SalI/NotI site of pCMV-SPORT6 plasmid vector The DH10B E. SalI/NotI site of pCMV-SPORT6 plasmid vector size is about standard chemical method. The average insert size is about 3.0kb. The library was constructed by Yulan Piao."
                                                      93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: Sall; site_2: Not1; Mouse cDNA project by the Laboratory of genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lggun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. This is a long-transcript enriched cDNA library (Ref. genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total Genome Res. 11: 1553-1558 (2001) for the postory of the postcolum. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: Oligo(dT) p
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/dev_stage="whole embryo including extraembryonic tissues
at 9.5-days postcoitum"
/lab_host="DH10B"
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/strain="C57BL/6J"
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/clone="NIA:B0346C06 IMAGE:30433469"
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Query Match Best Local Similarity

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Score 218.4; DB 1 Pred. No. 5.6e-33; Mismatches

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Indels Length

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1 (bases 1 to 855)
Hunter, C. and Elgar, G.
Alpha2 adrenergic receptor gene
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    AAM52117
AAE00990
AAE26634
ABP81780
AAM52118
AAE00989
AAE26633
AAR14149
AAW11804
                                                                                                                                                                                                                                                                       SUMMARIES
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Human alpha-2BAR t
Human alpha-2B-adre
Human alpha-2B-adr
Human alpha-2b-adr
Human alpha-2BAR t
Human alpha-2B-adre
Human alpha-2B-adr
Human alpha-2b beta
Human alpha-2b adr
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322331116
322331117
                                                                                                                                                                                                                                                                                                                                  Domain
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                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
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20	20	21	21	21	21	23	23	23	23	25	25	25	25	25	26	26	26	26	29	29	120	120
4.4	4.4	4.7	4.7	4.7	4.7	5.1	5.1	5.1	5.1	5.6		5.6		5.6				5.8		6.4 4	26.7	26.7
307	307	334	334	330	330	99	99	26	24	450	450	450	330	330	461	461	458	457	29	29	330	330
24	22	17	15	17	15	17	15	19	19	24	22	22	17	15	24	22	15	22	24	23	17	15
ABG73538	AAU08334	AAW02673	AAR48701	AAW02670	AAR48698	AAW02983	AAR50791	AAW39948	AAW39955	ABP81779	AAM52123	AAM52122	AAW02672	AAR48700	ABP81781	AAM52124	AAR54834	AAM52126	ABP53986	ABU67205	AAW02671	AAR48699
Human alpha2-adren	-	-	_	-			G-protein coupled	ef	Peptide effecting	$\mathbf{r}$	Human alpha-2AAR v	Human alpha-2AAR p	G-protein coupled	G-protein coupled	Human alpha 2c-adr	Human alpha-2CAR p	Human derived adre	Human alpha-2CAR v	Human alpha 2B adr			G-protein coupled

## ALIGNMENTS

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RESULT 1
AAM/52117
AAM/52117
ID AAM/5
XX AAM/5
XX AAM/5
XX Huma
XX Huma
XX Huma
XX Phose
XX P
                                                                                                                                                                           17-APR-2000; 2000US-0551744.
10-AUG-2000; 2000US-0636259.
19-OCT-2000; 2000US-0692077.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adarenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity; phosphorylation; inositol phosphate; alpha-2BAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM52117 standard; Protein; 450
Liggett SB,
                                                                                                                                                                                                                                                                                                                     17-APR-2001; 2001WO-US12575
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200179561-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human alpha-2BAR third intracellular loop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-FEB-2002 (first entry)
                                                                        (LIGG/) LIGGETT S
(SMAL/) SMALL K M.
       Small KM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= polypmorphic_site
373..396
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167..399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= polymorphic_site
/note= "Polymorphic site absent in the variant protein
(AAM52118)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC (b) detecting a polymorphic site comprising nucleotide positions 901-909 CC of (I), a site comprising cytosine or guanine at position 753 of (IIV) CC or a site comprising cytosine or guanine at position 753 of (IIV) CC or a site comprising (A) (99990999000) or (B) (99990909000) at CC or a site comprising (A) (99990990000) or (B) (99990909000) at CC or a site comprising cytosine or guanine at position 753 of (IIV) CC positions 961-972 of (III). The method may be used for genotyping an CC whether an individual is at increased risk of developing a disease comprising a disease selected from cardiovascular CC associated with alpha2B, alpha2A or alpha2, comprising detecting a CC disease, central nervous system disease and combinations of these. In the technique may be used to predict an individual's response CC disease, central nervous system disease and combinations of these. In the alpha2B, or alpha2C agonist (e.g. epinephrine, cloudine, oxymetazoline, guanabenz, UKI4304, BHT933 and CC combinations of these) or antagonist (e.g. cyohimbine, prazosin, ARC 239, CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate CC the human alpha-2BAR protein, the sequence is that of the third intracellular loop of colymorphic site at residues 301-303 (EEE), absent in the alpha-2BAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (a) obtaining a sample having a polymorphic site, comprising; alpha2A or alpha2C or fragment or complement of; and (b) detecting a polymorphic site, comprising; (b) detecting a polymorphic site and of (1) a site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting a polymorphic site -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; Page 146-147;
                                                                   361
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)B; AAI99905.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MDHQDPYSVQATAAIAAAITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADIL
LNPVIYTIFNQDFRRAFRRILCRPWTQTAW
                                                                              AQLTREKRETEVLAVVIGVFVLCWEPFFESYSLGAICPKHCKVPHGLFQFFFWIGYCNSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                        EEEEEEEECEPQAVPVSPASACSPPLQOPQGSRVLATLRGQVLLGRGVGAIGGQWWRRR
                                                                                                                               EEEEEEÉÉÉÉÉCEPQAVPVSPASÁCSPPLQQPQGSRVLATLRGQVLLGRGVGATGGQWWRRR
                                                                                                                                                                                                                                     ASAREVNGHSKSTGEKBEGETPEDTGTRALPPSWAALPNSQQQKEGVCGASPEDEAEBE
                                                                                                                                                                                                             ASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGOGOKEGVCGASPEDEAEEE
                                                                                                                                                                                                                                                                                                                   FFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALASV
                                                                                                                                                                                                                                                                                                                                                                                                NSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGS
                                                                                                                                                                                                                                                                                          FFAPCLIMILVYLRÍYLIAKRSNRRGÞRÁKGGÞGÓGESKOÞRÞÐHGGÁLÁSÁKLÞÁLÁSV
                                                                                                                                                                                                                                                                                                                                                                      NSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQBAWYILASSIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   VATLII PESLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MDHQDPYSVQATAAIAAAITFLILFTIFGNALVILAVLTSKSLRAPQNLFLYSLAAADIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         450 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                relates to genotyping an alpha-2B, 2A, (I)-(III) by detecting a polymorphic s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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Pred. No. 0;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        450;
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밁 5

1 MDHQDPYSYQATAAIAAAITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADIL

MDHQDPYSVQATAAIAAAITFLILFTIFGNALVILAVLTSKSLKAPQNLFLVSLAAADIL

60

Matches Query Match Best Local :

Similarity

100.0%; nilarity 100.0%; Conservative 0

0;

Score 450; D Pred. No. 0; 0; Mismatches

DB 22; 0;

Length

0

Gaps

Sequence

450

β

300 300

240

180

120

60 60 0

120

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RESULT 2
AABOO990
XX
AABOO990
XX
AABOO990
XX
AABOO990
XX
AABOO990
XX
AABOO990
XX
Huma
XX
Huma
XX
Huma
XX
Huma
XX
Homo
XX
Homo
XX
Homo
XX
FY
FT
Regi
FT
FT
PT
VX
PN
W020
PX
ED
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                               The present sequence is human alpha2B-adrenoceptor (alpha2B-AR) protein. Alpha2B-AR has a glutamic acid repeat element (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino acids (amino acids polypeptide. Alpha2B-AR gene is located on chromosome 2. Alpha2B-AR polypeptide. Alpha2B-AR gene is located on chromosome 2. Alpha2-AR norepinephrine and epinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating a mammal suffering from vascular contraction of coronary arteries and a disease involving vascular contraction of coronary arteries which is clinically expressed as coronary heat disease (CHD), unstable chronic angina pectoris which is clinically expressed as coronary heat disease prinzmetal's variant form or acute myocardial infarction (AMI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Snapir A,
Scheinin N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of coronary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAD04762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-OCT-2000; 2000WO-FI00913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR; glutamic acid repeat; intracellular loop; chromosome 2; catecholamine norepinephrine; pelnephrine; therapy; vascular contraction; coronary artery; coronary heat disease; CHD; chronic angina pectoris; acute myocardial infarction; AMI; Prinzmetal's variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (JUVA-) JUVANTIA PHARMA LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200129082-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human alpha2B-adrenoceptor (alpha2B-AR) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE00990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 29-31; 37pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
298..309
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T, Lakka
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Nyyssoenen
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1en K;
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RESULT 3
AAE26634
ID AAE2
XX AAE2
XX AAE2
XX Huma
XX Huma
XX Huma
XX Homc
XX Homc
XX Homc
XX Homc
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                                                               The invention relates to a method for detecting a risk of hypertension by determining the pattern of alleles encoding a variant alpha-2B-adrenoceptor (AR) protein. The methods and compositions of the invention are useful for detecting risks and targeting treatment for hypertension. The kit is also useful for selecting for clinical drug trials testing the matchine.
                                                                                                                                                                                                                                                                      Detecting a risk of hypertension and targeting by determining the pattern of alleles encoding alpha-2-adrenoceptor -
                                                                                                                                                                                                                                                                                                                   Detecting
                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-667063/71.
N-PSDB; AAD26634.
                                                                                                                                                                                                                     Disclosure; Page 30-31; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human alpha-28-adrenoceptor protein.
                           alpha-2B-adrenoceptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (JURI-)
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Pred. No. 0;
0; Mismatches
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Rough

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The present invention describes antigenic peptides (1) comprising:
CC (a) any one of 1601 sequences (see ABP82019 to ABB93619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular
CC and (2) an isolated antibody having high specificity and high affinity
CC or avidity for a particular GPCR. (1) can be used as GPCR modulators and
CC an antibodies. The antigenic peptides for GPCRs are useful in detecting
CC antibodies. The peptides and antibodies are also useful for detecting the
CC gresence or absence of corresponding GPCRs. The antigenic peptides for
CC gresence or absence of corresponding GPCRs. The antigenic peptides for
CC gresence or absence of corresponding GPCRs. The antigenic peptides for
CC diseases, or autoimmune diseases, growth-related designing drugs for
CC diseases, or autoimmune diseases, growth-related cell proliferative
CC atherosciterosis, bacterial, fungal, protozoan or viral infections,
CC diseases, parkinson's disease, multiple sclerosis, paraft versus host
CC diseases, parkinson's disease, multiple sclerosis, pain, psoriasis,
CC consist, depression, schizophrenia, dementia, mental retardation, memory
CC any other disorder in which GPCRs are involved. The antibodies may be
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention.
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Best Local Simi
Matches 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
361 A 361
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        ASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEEE
                                                                                              PPAPĆĽIMIĽVÝĽŘÍÝĽIAKRSNŘŘĠPRAKGGPGOGESKÓPŘPDHGGALASAKĽPALASV
                                                                                                                                                               FPAPCLIMILVYLRIYLIAKRSNRRGERAKGGPGQGESKQPREDHGGALASAKLPALASV
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                                                                                                                                                                                                       NSKRTPŘŘÍKČI ILTVÁLIAAVI SLPPLIYKGDOGPOPŘGRPOČKLNOBAMYTLASSIGS
                                                                                                                                                                                                                            NSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGS
                                                                                                                                                                                                                                                                                          VATLIIPFSLANELLGYWYFRRTWCEVYLALDVLPCTSSIVHLCAISLDRYWAVSRALEY
                                                                                                                                                                                                                                                                      450 AA;
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Pred. No. 0;
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The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic (2 receptor gene (1)-(III) by detecting a polymorphic site, comprising; (2 (a) obtaining a sample having a polymucleotide encoding an alpha-2B, CC alpha2A or alpha2C or fragment or complement of; and CC of (1), a site comprising cytosine or guanine at position 753 of (IIV) CC or a site comprising (A) (939939309) or (B) (93939353) at (IIV) CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine CC alsociated with alpha2B, alpha2A or alpha2 for gene and further used to determine CC disease, central nervous system disease and comprising detecting a CC disease, central nervous system disease and comprising detecting a CC disease, central nervous system disease and combinations of these. In CC disease, contral nervous system disease and combinations of these or an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, CC combinations of these) or antagonist (e.g. epinephrine, CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, CC combinations of these or antagonist (e.g. yohimbine, prazosin, ARC 239, CC cyclase, MAP kinase activity, phosphorylation or inscitol phosphate to a cyclase, MAP kinase activity, phosphorylation or inscitol phosphate CC the human alpha-2BAR variant protein, the sequence is that of the third intracellular loop of the human alpha-2BAR variant protein, the sequence is detected for the 3
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AAM52118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting a polymorphic site -
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; Page 147-149; 163pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-611728/70.
N-PSDB; AAI99906.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-APR-2000; 2000US-0551744.
10-AUG-2000; 2000US-0636259.
19-OCT-2000; 2000US-0692077.
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370..393
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Best Local
                                              Snapir A, He
Scheinin M,
                                                                                                                                                                                                                                                norepinephrine; epinephrine; therapy; vascular contraction; variant; coronary artery; coronary heat disease; CHD; chronic angina pectoris; acute myocardial infarction; AMI; Prinzmetal's variant.
                                                                                                                                                                                                                                                                               Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR; glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
           WPI; 2001-300318/31.
N-PSDB; AAD04761.
                                                                                                                                                                                                                                                                                                                                   04-JUL-2001
                                                                                                                         20-OCT-2000;
                                                                                                                                             26-APR-2001.
                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                             Human alpha2B-adrenoceptor (alpha2B-AR) variant protein
                                                                                                                                                                                                                                                                                                                                                        AAE00989
                                                                                                                                                                                                                                                                                                                                                                           AAE00989 standard; Protein;
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                                      Heinonen P, A
M, Salonen JT,
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                                                                                                                                                                                               Location/Qualifiers 298..306
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                                                           Alhopuro P,
                                        Valkonen
                                        Tuomainen T,
Valkonen V;
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0; Mismatches 0
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T, Lakka
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Matches 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein. Alpha2B-AR has a glutamic acid repeat element (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino acids (amino acids 294-311), located in the third intracellular loop of the receptor polypeptide. The variant is obtained by deletion of three glutamates from the Glu repeat (amino acids 307-309). Alpha2B-AR gene is located on chromosome 2. Alpha2-AR mediate many of the physiological effects of the catecholamines, norepinephrine and epinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating a mammal suffering from vascular contraction of coronary arteries and a disease involving vascular contraction of coronary arteries which is clinically expressed as coronary heat disease (CHD), unstable chronic angina pectoris which is clinically expressed as Prinzmetal's variant form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of coronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; Page
                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
 301
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BEEBEE 306
                                                             ASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGQGQXEGVCGASPEDEAEEE 300
                                                                                                                                      FFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALASV
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                                        ASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEEE
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                                                                                                                                                                                                                                                                                                                                                                                                              68.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence is human alpha2B-adrenoceptor (alpha2B-AR) variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-27; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                  <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                              Score 306; DB 22;
Pred. No. 1e-270;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                  <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                      120
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                                          300
                                                                                                               240
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RESULT 7
AABZ6633
ID AABZ
XX AABZ
XX AABZ
XX Huma
XX Huma
XX Huma
XX Hype
XX Synt
XX Synt
XX PD WO20
PN WO20
PD 29-A
                                                     Homo sapiens
Synthetic.
                                                                                               Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;
                                                                                                                                         13-DEC-2002
                                                                                                                                                                                    AAE26633 standard; Protein;
                                                                                                                    Human alpha-2B-adrenoceptor variant
                                                                                     hypertension;
                                                                                                                                         (first entry)
                                                                                     hypotensive;
                                                                                                                                                                                      447
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EBEBEE

WO200266617-A1

29-AUG-2002

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Query Match
Best Local S
Matches 306
                         01-OCT-1991
                                              US5053337-A.
                                                                        Homo sapiens
                                                                                    Neurotransmission; adrenaline; epinephrine; NGC-alpha2beta.
                                                                                                                 Human alpha 2 beta adrenergic receptor.
                                                                                                                                                    06-JAN-1992
                                                                                                                                                                                              AAR14149 standard; Protein; 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by determined adrenoceptor (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method for detecting a risk of hypertension by determining the pattern of allels encoding a variant alpha-2B-adrenoceptor (AR) protein. The methods and compositions of the invention are useful for detecting risks and targeting treatment for hypertension. The kit is also useful for selecting for clinical drug trials testing the antihypertensive effect of compounds. The present sequence is human alpha-2B-adrenoceptor variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 26-27; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting a risk of hypertension and targeting treatment
by determining the pattern of alleles encoding a variant
alpha-2-adrenoceptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-667063/71.
N-PSDB; AAD44388.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306;
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                                                                                                                                                                                                                                                                      BEEEEE
                                                                                                                                                                                                                                                                                           EEEEEE 306
                                                                                                                                                                                                                                                                                                                        ASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGQGKEGVCGASPEDEAEEE
                                                                                                                                                                                                                                                                                                        ASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGGGOKEGVCGASPEDEAEEE
                                                                                                                                                                                                                                                                                                                                                          FPAPCLIMILVYLRÍYLÍAKRSNKRGÞRAKGGÞGGGESKÓÞRÞÐHGGALASAKLÞALASV
                                                                                                                                                                                                                                                                                                                                                                          NSKRTPRRİKCIİLTVWLIAAVISLPPLIYKGDOGPOPRGRPQCKLNQEAWYILASSIGS
                                                                                                                                                                                                                                                                                                                                                                                                                             NSKRTERRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQBAWYILASSIGS 180
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                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  447 AA;
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                                                                                                                                                                                                                                                                    306
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                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 447;
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         30-OCT-1989;
30-MAY-1991;
22-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 234; Conserv
                                                                                                                                                              Alpha-2b adre epinephrine;
                                                            22-OCT-1992;
                                                                                     21-JAN-1997
                                                                                                              US5595880-A
                                                                                                                                      Homo sapiens
                                                                                                                                                                                              Human alpha-2b adrenergic receptor.
                                                                                                                                                                                                                                 25-MAR-2003
06-MAY-1997
                                                                                                                                                                                                                                                                      AAW11804;
                                                                                                                                                                                                                                                                                           AAW11804 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone NGC-alpha2beta was isolated from a human spleen genomic library by screening with a fragment of the human 5-HTIA receptor gene. The gene was used to express recombinant receptor protein which can be used to produce antibodies for inhibition of receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated DNA encoding human adrenergic receptor - for detanucleic acids encoding alpha, 2-beta adrenergic receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1991-310087/42.
N-PSDB; AAQ14151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weinshank RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-OCT-1989;
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                                                                                                                                                                                                                                                                                                                                                                                               285 GHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGOGOKEGVCGASPEDEABEEEEEEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 MILVYLRIYLIAKRSNRRGFRAKGGPGQGESKQPRPDHGGALASAKLPALASVASAREVN
                                                                                                                                                                                                                                                                                                                                                                                                                                         248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 RÍKCIÍLÍTVMLÍJAAVÍSLÞÞLÍYKGDÓGÞÓÞRGRÞÓCKLNÓBÁMVÍLASSÍGSFFAÞCLÍ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 RIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQBAWYILASSIGSFFAPCLI
                                                                                                                                                 adrenergic receptor; adrenoceptor; adrenaline;
ine; signal transduction; neurotransmitter; ligand.
                                                                                                                                                                                                                                                                                                                                                                EECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRA 361
                                                                                                                                                                                                                                                                                                                                               EECEPQÁVPVSPÁSÁCSPPLQOPQGSRVLÁTLKGOVLLGRGVGÁIGGQWWRRRA
                                                                                                                                                                                                                                                                                                                                                                                                               GHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGOGOKEGVCGASPEDEAEEEEEEEEEEEE 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIĹVÝĽŘÍ ÝĽIÁKŘŠNŘŘGÉŘAKGÓPGQGESKÓPŘÞDHGGÁĽÁSÁKĽÞÁĽÁSVÁSAŘEVN
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     89US-0428856.
91US-0707604.
92US-0965040.
                                                                                                                                                                                                                            (updated)
(first entry)
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                                                         9208-0965040
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                                                                                                                                                                                                                                                                                          Protein;
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100.0%; Pr
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Gaps

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344

247 224 Ś

RESULT 8
AAR14149
ID AAR1
XX AAR1
XX AAR1
XX AAR1
XX O6-J
XX Huma
XX Huma
XX Neur
XX Neur
XX Neur
XX Neur
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XX US50
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301 301 241 241 181 181 121

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RESULT 10
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Best Local
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                                                                                                                                                                                              G-protein coupled receptor; ligand binding assay; transmembrane domain psychotic disorder; schizophrenia; dopamine; cAMP; adenosine; thrombin muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human alpha-2B adrenergic receptor (AAW11804) is a member of the rhodopsin-like signal transducer family. Its amino acid sequence was deduced from a genomic DNA clone (AAT59499) obtd. from a human spleen DNA library. Vectors have been adapted to allow prodn. of alpha-2B adrenoceptor in bacterial, yeast or mammalian cells; transfected Ltk- cells, designated L-NGC-alpha-2B, are deposited as ATCC CRL 10275. Membranes of transfected amammalian cells can used in novel methods to identify drugs which specifically interact with, and bind to, the alpha-2B adrenergic receptor. (Updated on 25-MAR-2003 to correct PF field.)
                                        10-SEP-1992;
                                                                                                                                                                                                                                                                                      05-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cells expressing recombinant receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assay for alpha-2b adrenergic receptor ligands - using membranes
             VIND ( ANAM)
                                                                                                 17-MAR-1994.
                                                                                                                            WO9405695-A1.
                                                                                                                                                                                  rhodopsin; opsin;
                                                                                                                                                                                                                                                                                                                  AAR48699
                                                                                                                                                                                                                                                                                                                                             AAR48699 standard; Protein; 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAT59499.
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                                                                                                                                                       sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                     345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 RIKCIILTVMLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGSFFAPCLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             EECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRA 361
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             NEW YORK STATE
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                                        92US-0943236
                                                                    93WO-US08528
                                                                                                                                                                                   odorant; cytomegalovirus.
                                                                                                                                                                                                                                                      human alpha-2 C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.0%;
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; Pred. No. 6.2e-205;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                        adrenergic receptor protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 487;
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                                                                                                                                                                                                              thrombin;
                                                                                                                                                                                                                             domain;
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RESULT 11
AAW02671
ID AAW02671
AAW02671
AAW02671
AC AAW02
XX AAW02
AC AAW02
XX 25-MA
DT 12-MO
XX 6-pro
XX G-pro
KW G-pro
KW G-pro
KW G-pro
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KW G-pro
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KW G-pro
KW G-pro
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XX US550
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Best Local Similarity
Matches 120; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      odorant, cytomegaloviral and other G-protein coupled receptors. The receptor proteins were used to design polypeptides, pref. based on the transmembrane domains, for use in G-protein coupled receptor ligand binding assays. The polypeptide fragments retain biological activity such as binding a GPR ligand or modulating GPR ligand binding to a GPR such as binding a GPR ligand or modulating GPR ligand binding to a GPR see AAR48759-R48758, AAR50569-R50807 and AAR89189-R89195 for examples of polypeptide fragments can be used in compositions for treating subjects suffering from a pathology related to a GPR abnormality e.g. a psychotic disorder such as schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G-protein coupled receptor; ligand binding assay; transmembrane domain; schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G-protein coupled human alpha-2 C2 adrenergic receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       odorant; cytomegalovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         schizophrenia; dopamine; cAMP; adenosine; thrombin; adrene; muscarinic acetylcholine; endothelin; bombesin; endocrine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW02671;
                           New dopamine receptor peptide - useful as antipsychotic agent, e.g. for treating schizophrenia
                                                                                                                        WPI; 1996-208785/21.
                                                                                                                                                                                                                                                                                                  09-SEP-1993;
10-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                     09-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5508384-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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12-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW02671 standard; peptide; 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptides of G-coupled receptor proteins (
binding GPR ligands or modulating GPR binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murphy RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                16-APR-1996
                                                                                                                                                                                                                                       (UYNY ) UNIV NEW YORK STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55
                                                                                                                                                                                   RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRALEYNSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYIL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR48685-R48758 represent a range of G-protein coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRALEYNSKRIPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYIL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAADILVATLIIPESLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAADILVATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           330 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 72-73; 160pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schuster DI;
                                                                                                                                                                                   Schuster DI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (updated)
(first entry)
                                                                                                                                                                                                                                                                                                  93US-0118270.
92US-0943236.
                                                                                                                                                                                                                                                                                                                                                                                        93US-0118270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from cAMP, adenosine, muscarinic acetylcholine, pin, endothelin, bombesin, endocrine, rhodopsin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                serotonergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 120; DB 15;
Pred. No. 5.4e-101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GPRs) - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for
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Disclosure; Column

69-72; 184pp; English

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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              odorant, cytomegaloviral and other GPR proteins. The receptor proteins were used to design polypeptides, pref. based on the transmembrane domains, for use in G-protein coupled receptor ligand binding assays. The polypeptide fragments retain biological activity such as binding a GPR ligand or modulating GPR ligand binding to a GPR (see AAW02747-W02999 for examples of polypeptide fragments). The polypeptide fragments can be used in compositions for treating subjects suffering from a pathology related to a GPR abnormality e.g. a psychotic disorder
                                                                    Modified G-protein coupled receptor useful for identifying inverse agonist or antagonist of the receptor, comprises a
                           Disclosure; Fig 2; 57pp;
                                                      inverse agonist
terminal having
                                                                                                                   WPI; 2002-690758/74
                                                                                                                                               Oakley RH, Barak LS,
                                                                                                                                                                                           (BARA/)
                                                                                                                                                                                                                                                  03-NOV-2000;
08-JAN-2001;
                                                                                                                                                                                                                                                                                           05-NOV-2001; 2001US-0993844.
                                                                                                                                                                                                                                                                                                                          08-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                       US2002106739-A1
                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                              Human; G-protein coupled receptor; receptor; GPCR; palmitoylation site; phosphorylation cluster; arrestin; endosome; angina pectoris; rhinitis; atherosclerosis; asthma; emphysema; inflammatory disease; glaucoma; pain; rheumatoid arthritis; obesity; Parkinson's disease; rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G-protein coupled receptor (GPCR) fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU67205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU67205 standard; Peptide; 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GPR) proteins selected from cAMP, adenosine, muscarinic acetylch adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proteins AAW02657-W02720
                                                                                                                                                                                                                        (OAKL/)
                                                                                                                                                                            (CARO/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Updated on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44
                                                                                                                                                                          OAKLEY R H.
BARAK L S.
LAPORTE S A.
CARON M G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     schizophrenia.
d on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAADILVATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SRALEYNSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRALEYNSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAADILVATLIIPESLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          330 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                  2000US-245772P.
2001US-260363P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                        or antagonist
one or more c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.7%;
                                                                                                                                                                                                                                                                                                                                                                                                            obesity; Parkinson's
                                                                                                                                               Laporte
                           English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 represent a range of G-protein coupled receptor cAMP, adenosine, muscarinic acetylcholine,
                                                         clusters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 120; DB 17; I
; Pred. No. 5.4e-101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                               SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                               Caron MG
                                                        receptor, of phosph
                                                        phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #4
                                                                                                                                                                                                                                                                                                                                                                                                            disease; rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                      carboxyl
                                                                                   an agonist,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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The invention relates to a modified G-protein coupled receptor (GPCR

Disclosure; Page 24; 42pp; English

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RESULT 13
ABP53986
ID ABP53
XX ABP53
XC ABP53
XC ABP53
XX Humar
XX G prc
KW G prc
KW phote
XX Phomo
XX Homo
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                  Detecting G-protein-coupled receptor pathway activity comprises treating a cell having G-protein-coupled receptor activity with a test compound, obtaining a digital image of the cell and detecting position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G protein-coupled receptor; GPCR; detection;
                                                                                                 of conjugated proteins
                                                                                                                                                                                                                                                                       WPI; 2003-018747/01.
                                                                                                                                                                                                                                                                                                                                      Barak LS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-2001; 2001US-275339P.
12-MAR-2002; 2002US-0095620.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        digestion; pain; fluid electrolyte balance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          photo-transduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human alpha 2B adrenergic receptor class A GPCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP53986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP53986 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-MAR-2002; 2002WO-US07434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                           (UYDU-) UNIV DUKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200273199-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprising an NPXXY motif, and a carboxyl terminal tail which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               422 NPVIYTIFNODFRRAFRRILCRPWTQTAW 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NPVIYTIFNODFRRAFRRILCRPWTQTAW 29
                                                                                                                                                                                                                                                                                                                                  Oakley RH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Α
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurotransmission; vascular tone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 23; |
8.5e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor; olfaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 29
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RESULT 14
AAM52126
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a method for detecting G protein-coupled receptor (GPCR) pathway activity. The method comprises: (1) providing at least one cell expressing GPCR and conjugated proteins; (2) treating the cell with a test compound; (3) obtaining a digital image of the cell by detecting and measuring energy emitted from the detectable molecules; and (4) detecting the localization of some of the conjugated proteins at one of endocytic vesicles and endosomes. The method can be used for detecting compounds that activate GPCR-activity in vivo and in vitro, where the including photo-transduction, olfaction, neurotransmission, vascular tone, cardiac output, digestion, pain and fluid electrolyte balance. The present sequence represents a GPCR amino acid sequence which is given in the exemplification of the present invention.
Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing disease associated with the corresponding receptor comprises detecting a polymorphic site -
                                                                                                                                                                                                                                                                                                                                              17-APR-2000; 2000US-0551744.
10-AUG-2000; 2000US-0636259.
19-OCT-2000; 2000US-0692077.
                                                                                                                                                                                                                                                                    (LIGG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity; phosphorylation; inositol phosphate; alpha-2CAR.
                                                                                                                                     WPI; 2001-611728/70.
N-PSDB; AAI99933.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-APR-2001; 2001WO-US12575.
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larity 100.0%;
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208..231
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                           corresponding receptor comprises detecting
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Claim 78; Page 160-162; 163pp; English

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RESULT 15
AAR54834
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CT O1-FE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local :
                           N-PSDB; AAQ64890
                                                                 WPI; 1994-185923/23.
                                                                                                                                                                                                                                                                                                                                  06-MAY-1994.
                                                                                                                                                                                                                                                                                                                                                                                                   JP06121686-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human derived adrenaline alpha 2CII receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergy receptor gene (I)-(III) by detecting a polymorphic site, comprising; (a) obtaining a sample having a polymucleotide encoding an alpha-2B, alpha-2B or alpha-2C or fragment or complement of; and alpha-2C or fragment or complement of;
                                                                                                                                                                                            12-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                           (ASAH ) ASAHI KASEI KOGYO KK
                                                                                                                                                                                                                                                          12-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adrenaline receptor; alpha CII; screening; detection; pharmocology;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 VYLALDVLFCTSSIVHLCAISLDRYW 151
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                                                                                                                                                                                            92JP-0272744.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "may or may not be present, but
present if amino acid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "may or may not be present"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present"
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Adrenaline receptor gene encoding alpha 2CII receptor for screening drugs reactive to the alpha 2CII receptor XX Claim 1; Page 9-11; 13pp; Japanese.

XX AAQ64890 encodes the amino acid sequence of a polypeptide CC (AAR54834) that constitutes human derived adrenaline alpha 2CII CC receptor. The DNA can be used for the study of the pharmacological CC importance of the gene expression in humans.

XX SQ Sequence 458 AA;

Query Match 5.8%; Score 26; DB 15; Length 458; Best Local Similarity 100.0%; Pred. No. 4.8e-15; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

87 VYLALDVLFCTSSIVHLCAISLDRYW 112

Db 126 VYLALDVLFCTSSIVHLCAISLDRYW 151

Search completed: February 6, 2004, 18:23:31

Job time: 38.6254 secs
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Patent No. 5508384
GENERAL INFORMATION:

NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:

APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF

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Regult
No.
RESULT 1.
US-08-118-270-20
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Perfect score:
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Maximum DB
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and is der
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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US-08-103-170-17
US-07-741-453A-46
US-08-118-270-21
PCT-US93-08528-21
US-08-186-9718-4
US-08-194-338-5
US-08-194-338-5
US-08-196-9898-11
US-08-144-734A-1
US-08-1818-270-332
US-08-118-270-332
US-08-118-270-22
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US-08-118-270-22
US-08-118-270-22
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PCT-US93-08528-20
                                                                ALIGNMENTS
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1265.095 Million cell updates/sec
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21, Appli

21, Appli

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Seguence

20,

Application US/08118270

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-118-270-20
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PCT-US93-08528-20
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                                                                                                                              Sequence 20, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity
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TELEX: 248633
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/118
RETIING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943
PRILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: TOWNBERI, KEVIN G.
REGISTRATION NUMBER: 34,033
REGISTRATION NUMBER: MIRES
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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STREET: Washington
CITY: Washington
CTATE: D.C.
TTATE: D.C.
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TELECOMMUNICATION INFORMATION:
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                                                                                                              STREET: 419 Sever CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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                                                                                                 D.C
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419 Seventh Street, N.W.,
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OPERATING SYSTEM:

PC-DOS/MS-DOS

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PCT-US93-08528-20
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Patent No. 5474898
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Best Local Similarity
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                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,338
FILING DATE: 08-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,174
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Venter, John C.
APPLICANT: Fraser, Claire M.
APPLICANT: MCCOmbie, William R.
TITLE OF INVENTION: OCTOPAMINE RECEPTOR
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PILING DATE: 09-SEP-PRIOR APPLICATION NUMBER:
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REFERENCE/DOCKET NUMBER: NIH101.001DV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 215-055
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAADILVATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAV 103
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100.0%; Pred. No. 2.6e-91;
tive 0; Mismatches 0;
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                                                                                                    TELEFAX: (703)486-2347
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/63
FILING DATE: 24-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul
REGISTRATION NUMBER: 31,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Recombinant Genomic Clones Encoding TITLE OF INVENTION: Histamine H1, H2, and H3 Receptors, TITLE OF INVENTION: Thereof, and Proteins Encoded Therei
                FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                   TOPOLOGY: 1i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.0%; hes 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Arlington STATE: Virginia COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                   REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 23
                                                                                       TYPE:
                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: P.C.
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 ORGANISM:
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                                                                                     amino acid
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Homo sapiens
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Thereof, and Proteins Encoded Therefrom
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L00.0%; Pred. No. 1.3e-13;
                                                                                                                                                                                                                                                                                                                           US 07/633,060
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                                                                                                                                              17:
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Query Match

5.6%;

Score 25;

DB 2

Length 27;

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RESULT 6
US-08-118-270-21
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                                                                                                                      Sequence 21, Application US/08118270 Patent No. 5508384
                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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              GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 56 amino acids
TYPE: AMINO ACID
STRANDEDNESS: Bingle
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (202) 861-30
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1615 L.C. CITY: WASHINGTON, D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 19911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                    88 YLALDVLFCTSSIVHLCAISLDRYW 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 VYLALDVLFCTSSIVHLCAISLDRY 111
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                                                                                                                                                                                                                                YLALDVLFCTSSIVHLCAISLDRYW 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VYLALDVLFCTSSIVHLCAISLDRY 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/07741453A
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LIBERT, FREDERIC
DUMONT, JACQUES
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                                                                                                                                                                                                                                                                                                                                                                                      peptide
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ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
                                                                                                                                                                                                                                                                                                   5.6%; Score 25; DB 3;
100.0%; Pred. No. 1.4e-
ltive 0; Mismatches
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PCT-US93-08528-21
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GENERAL INFORMATION:
APPLICANT: New York University
                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
PILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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TITLE OF INVENTION: RE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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REFERENCE/DOCKET NUMBER: MUI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
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CURRENT APPLICATION DATA:
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Local Similarity 100.0%; I
hes 25; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MU
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TELEPHONE: 202-737-3528
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
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       MURPHY=2 PCT
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TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: not rele
MOLECULE TYPE: prote
US-08-465-971B-4
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                                           Query Match
Best Local Similarity 100.
25; Conservative
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US-08-465-971B-4
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                                                                                                                                                                                                                                CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J G.
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 3256
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                              ZIP: 07068-1739

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,971

FILING DATE: 06-JUN-1995
                                                                                                                                                                         TELEFAX: 201994-1744
[INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4,
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INFORMATION FOR SEQ ID NO:
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CORRESPONDENCE ADDRESS:
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les 25; Conservative
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TYPE: amino acid
STRANDEDNESS: single
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112 YLALDVLFCTSSIVHLCAISLDRYW 136
                        88 YLALDVLFCTSSIVHLCAISLDRYW 112
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E: Cecchi, Stewart & Olstein
6 Becker Farm Road
                                                                                                                                     not relevant
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/ENTION: Human G-Protein Receptor HIBEF51
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linear
                                                                                                                           protein
                                                                                                                                                   not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide
                                                 5.6%; bu
100.0%; Pr
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100.0%; Pro
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                                                  Score 25; DB; Pred. No. 7.1
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Pred. No.
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                                                                 DB 2; L
7.1e-13;
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                                                                            Length 358;
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                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/08196989B Patent No. 5585476
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
25; Conservative
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APPLICANT: Fraser, Claire M.
APPLICANT: MCCombie, William R.
TITLE OF INVENTION: OCTOPAMINE RECEPTOR
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, olson and Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
STATE: CA
STATE: CA
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FILING DATE: 28-MAR-1991
ATTORNEY AGENT INFORMATION:
NAME: IBTGelsen, Ned A.
REGISTRATION NUMBER: 29.655
REFERENCE/DOCKET NUMBER: NHI
TELECOMMUNICATION INFORMATION:
TELECHIONE: (619) 235-8550
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INFORMATION FOR SEQ ID NO:
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COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                  APPLICANT: MacLennan, TITLE OF INVENTION: M. TITLE OF INVENTION: G.
                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,338
FILLING DATE: 08-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
ADDITIONAL MINABED: THE OT/676 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acid
                                                             COUNTRY:
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                                                                                                                                                                                 ADDRESSEE:
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STRANDEDNESS: sir
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                                   32606
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                                                                                                                                    E: Saliwanchik & Saliwanchik
2421 N.W. 41st Street, Suite A-1
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NO: 5:
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G-Protein Coupled
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Pred. No.
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Receptors
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MEDIUM TYPE: COMPUTER: II

Floppy disk

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                                                                   APPLICATION NUMBER: US/08/444,734A FILING DATE: CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/029,917 FILING DATE: 03-MAR-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/548,714 FILING DATE: 06-JUL-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MCVittie, Loris D.
TITLE OF INVENTION: cDNA encoding the rat D1 dopamine
TITLE OF INVENTION: receptor linked to adnylyl cyclase activation and
TITLE OF INVENTION: expression of the receptor protein in plasmid-transfected
TITLE OF INVENTION: cell lines
                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: MA
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APPLICATION NUMBER: US/08/196,989B
FILING DATE: 15-FEB-1994
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                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Knobbe, Martens, Olson and Bear STREET: 620 Newport Center Drive, Sixteenth Floor CITY: Newport Beach
NAME: Altman, Daniel E. REGISTRATION NUMBER: 34, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U
ZIP: 92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
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Mahan, Lawrence C.
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     Daniel E.
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                              Matches
                                                             Query Match
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                                                                                                                                                                                                   TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 11:
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APPLICANT: MacLen
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,936
FILING DATE: December 6, 1996
CLASSIFICATION: 536
CLASSIFICATION: 536
                                                                                                          MOLECULE TYPE:
                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Pace, Doran R.
REGISTRATION NUMBER: 38,261
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Molecular Cloning and Expression of TITLE OF INVENTION: G-Protein Coupled Receptors NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                TELEPHONE: 352-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
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                                                Local
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                                                                                                                                     STRANDEDNESS:
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                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: MAC-100C1
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STRANDEDNESS: sin
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88 YLALDVLFCTSSIVHLCAISLDRYW 112
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                                              Similarity
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2421 N.W. 41st Street, Suite A-1
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                              Conservative
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                                                                                                        not relevant:
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                                              Score 25;
Pred. No.
                              Mismatches
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                                              DB 2; ; . 8.7e-13
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b. 8.7e-13;
                                                        Length 450;
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US-08-118-270-332
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SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                     Query Match
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US-09-225-024-11
                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  -09-225-024-11
                                                                                                                                                          tent No. 5508384
                                                 NUMBER OF SEQUENCES:
                                                                                                       APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Pace, Doran R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: MAC-100C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
                                                                     THE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN RECEPTORS, AND COMPOSITIONS AND M
                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 6-DEC-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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THE TOTAL TOTAL TOTAL TOTAL MACLEN
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                                         DDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MacLennan, A. John
TITLE OF INVENTION: Molecular Cloning and Expression of
TITLE OF INVENTION: G-Protein Coupled Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 15-FEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 04-JAN-1999
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/225,024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Washington : D.C.
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25; Conserv
         E: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
                                                                                                                                                                Application US/08118270
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2421 N.W. 41st Street, Suite A-1
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                                                                    AND METHODS THEREOF
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RESULT 15
PCT-US93-08528-332
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPARIABLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION
NAME: TOWNSEN: 34,033
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 5.1%; Score 23; DB 1; Length 99; Best Local Similarity 100.0%; Pred. No. 1e-11; Matches 23; Conservative 0; Mismatches 0; Indels
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SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPB: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                           REFERENCE DOCKET NUMBER: 34,033
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPAX: 702-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: New Yor
TITLE OF INVENTION:
TITLE OF INVENTION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: UFILING DATE: 10-SEP-1
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REFERENCE/DOCKET NUMBER: MURPHY=2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Townsend, Kevin G. REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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Y: USA
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419 Seventh Street, N.W., Suite 300
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332:
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Perfect score:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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Match
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                  /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
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.5 US-10-001-073-4
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Sequence 8, Appli
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## ALIGNMENTS

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; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo s
US-09-825-923-4
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US-09-825-923-4
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09825923 Patent No. US20010016338A1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Nyyss"nen, Kristiina
APPLICANT: Salonen, Riitta
APPLICANT: Salonen, Riitta
APPLICANT: Kauhanen, Jussi
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEO IN NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Snapir, Amir
APPLICANT: Heinonen, Pa
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Scheinin, Mika
Salonen, Jukka T
Tuomainen, Tomi-Pekka
LNPVIYTIFNQDFRRAFRRILCRPWTQTAW
                                                       AQLTREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPKHCKVPHGLFQFFFWIGYCNSS 420
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Alhopuro, Pia
Karvonen, Matti
Koulu, Markku
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100.0%; Pred. No. 0;
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RESULT 3
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Sequence 7, Application US/10001073
Publication No. US20030113725A1
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Liggett, Stephen
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
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; ORGANISM: Homo sapiens
US-10-077-870-4
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Publication No. US20030003470A1
GENERAL INFORMATION:
APPLICANT: Salonen, Jukka T
TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US/10/077,870
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: FI 20010323
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 3.1
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 450; Conservative 0; Mismatches
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Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: LifeSpan Blosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR PRILING DATE: 2000-12-19
PRIOR DATE: 2000-12-19
PRIOR DATE: 2000-12-19
PRIOR DATE: 2000-13-19
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US-10-225-567A-42
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; ORGANISM: Homo
US-10-001-073-7
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ORGANISM: Homo sapiens
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                                                                                                   h 80.2%; So Similarity 100.0%; F 61; Conservative 0;
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Pred. No. 0;
0; Mismatches
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; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo s
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APPLICANT: Valkonen, Vell-pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09825923 Patent No. US20010016338A1
                                                                                                                                              Matches
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Best Local Similarity
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APPLICANT: Heinon:
APPLICANT: Alhopu:
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                                              VATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEY 120
                                                                                                    MDHQDPYSVQATAAIAAAITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADIL 60
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Koulu, Marku
Pesonen, Ullamari
Scheinin, Mika
Salonen, Jukka T
Tuomainen, Tomi-Pekka
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Nyyse"nen, Kristiina
Salonen, Riitta
                                                                                                                                          68.0%; Score 306; DB 9; Lilarity 100.0%; Pred. No. 4.3e-242; Conservative 0; Mismatches 0;
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US-10-077-870-2
Sequence 8; Application US/10001073
Publication No. US20030113725A1
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
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Sequence 2, Application US/10077870
; Sequence 2, Application US2003003470A1
; GENERAL INFORMATION:
APPLICANT: Salonen, Jukka T
TITLE OF INVENTION: Method for detecting a risk of
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077,870
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: FI 20010323
; PRIOR APPLICATION NUMBER: FI 20010323
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 3.1
; SSOFTWARE: PatentIn Ver. 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-077-870-2
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 8

FILE REFERENCE: 13073-PCT

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                                                                                                                      ; SEQ ID NO 18
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Human
US-09-993-844-18
                                                                  Best Loc
Matches
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                                                                                             Query Match
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-001-073-8
                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/993,844
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: US 60/245,772
PRIOR FILING DATE: 2000-11-03
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/260,363
PRIOR FILING DATE: 2001-01-08
NUMBER OF SEQ ID NOS: 81
                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Modified G-Protein Coupled Receptors FILE REFERENCE: 033072-026
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Caron, Marc
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                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09993844
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                                                             Conservative
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                                                    6.4%; Pr/
100.0%; Pr/
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                                                       Score 29; DB; Pred. No. 2e-
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                                                                     DB 10;
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US-10-001-073-44

Sequence 44, Application US/10001073

Publication No. US20030113725A1

GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-44
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
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US-10-225-567A-44
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; ORGANISM: Homo sapiens
US-10-001-073-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTMARE: PatentIn version 3.1
SEQ ID NO 44
SEQ ID NO 44
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Publication No. US20030113798A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 46
TENORM: ACC
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Best Local Similarity
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APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
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1 Similarity 100.0%; F
26; Conservative 0;
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0; Mismatches
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5e-13;
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US-10-001-073-26
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                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-001-073-27
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US-10-001-073-26
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                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
LENGTH: 450
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Best Local Similarity 100.0%; P
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Best Local
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LENGTH: 450
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CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                               TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms FILE REFERENCE: 13073-PCT
                                                                                                                                                                                                                                                                            APPLICANT: Liggett, Stephen APPLICANT: Small, Kirsten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms FILE REFERENCE: 13073-PCT
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109 YLALDVLFCTSSIVHLCAISLDRYW 133
                  88 YLALDVLFCTSSIVHLCAISLDRYW 112
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                                                      100.0%; Pr
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Pred. No.
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. 3.2e-12;
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. 5e-13;
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                                                                                     Length 450;
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RESULT 14

Search completed: February Job time : 30.5987 secs

6, 2004, 18:28:03

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-795B-4
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                                                                                                Query Match 4.7%;
Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.1 SEQ ID NO 40
                                                                             Matches
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Best Local Similarity
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PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
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CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 07/273373
PRIOR FILING DATE: 1988-11-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/060,795B CURRENT FILING DATE: 2002-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Machida, Curtis A. TITLE OF INVENTION: Dopamine Receptors and Genes FILE REFERENCE: 90-1092-CCC
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                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 07/973588
PRIOR FILING DATE: 1992-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/238977 PRIOR FILING DATE: 1999-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Civelli Olivier APPLICANT: Bunzow, James
                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1989-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 08/474892
PRIOR FILING DATE: 1995-06-07
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                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 07/438544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 450
TYPE: PRT
ORGANISM: Homo sapiens
109
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                                   88 YLALDVLFCTSSIVHLCAISL 108
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YLALDVLFCTSSIVHLCAISL 129
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Burmer, Glenna C.
Roush, Christine L.
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                                                                               Conservative
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100.0%; Pred. No. 3.2e-
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                                                                                                Score 21; DB 15; Pred. No. 4.5e-0
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alpha-2B-adrenergic receptor - human

// Alternate names: alpha-2C2-adrenergic receptor

C/Species: Homo sapiens (man)

C/Species: Homo sapiens (man)

C/Date: 22-Uan-1993 #sequence revision 22-Jan-1993 #text_change 29-Oct-1999

C/Accession: A37223; I39407; S14308; A36158

R/Weinshank, R.L.; Zgombick, J.M.; Macchi, M.; Adham, N.; Lichtblau, H.; Br.
                                                                       RESULT 1
A37223
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Perfect score:
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N.; Lichtblau, H.; Branchek,

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A;Molecule type: DNA
A;Residues: $6-185 < CHH>
A;Residues: $6-185 < CHH>
A;Cross-references: GB:X59604; NID:g28635
A;Ote: this translation is not annotated in GenBank entry HS
A;Note: this translation is not annotated in GenBank entry HS
R;Chang, A.C.; HO, T.F.; Chang, N.C.
Biochem. Biophys. Res. Commun. 172, 817-823, 1990
A;Title: In vitro amplification by polymerase chain reaction
A;Reference number: A36158; MUID:91054503; PMID:2173582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 2p13-2q13
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled recept
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A;Residues: 95-361,'QL',364-389 <CHA>
A;Cross-references: GB:M38742; NID:g177867; PIDN:AAA62823.1; PID:g177868
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R;Lomasney, J.W.; Lorenz, W.; Allen, L.F.; King, K.; Regan, J.W.; Yang-Feng, Proc. Natl. Acad. Sci. U.S.A. 87, 5094-5098, 1990
A;Title: Expansion of the alpha 2-adrenergic receptor family: cloning and che A;Reference number: 139407; MUID:90311349; PMID:2164221
A;Accession: I39407
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A;Cross-references: GDB:120539; OMIM:104260
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A; Residues: 1-450 < LOM>
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                                                                          EEEEEEEECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRR 360
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alpha-2-C2 adrenergic receptor - mouse C; Species: Mus musculus (house mouse) C; Date: 22-Nov-1993 #sequence_revision C; Accession: S28221; JH0693
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C./Species: Rattus norvegicus (Norway rat)
C./Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 13-Aug-1999
C./Accession: I51883
R./Le Jossec, M. Cloix, J.F.; Pecquery, R.; Giudicelli, Y.; Dausse, J.P.
Am. J. Hypertens. 8, 177-182, 1995
A;Title: Differential sodium regulation between salt-sensitive and salt-res.
A;Reference number: I51883; MUID:95275492; PMID:7755946
A;Accession: I51883
                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X74400; NID:9840862; PIDN:CAA52411.1; PID:9940816 C;Superfamily: vertebrate rhodopsin C;Keywords: neurotransmitter receptor
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A; Residues: 1-448 < RES>
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C;Species: Rattus sp. (rat)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 30-May-1997
C;Accession: I53161
R;Wang, S:V; Pilkey, D.T.
Diabetes 43, 127-136, 1994
A;Title: Identification in islets of Langerhans of a new rat alpha 2-adrene A;Reference number: I53161; MUID:94085695; PMID:8262309
A;Accession: I53161
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Superfamily: vertebrate rhodopsin
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A; Residues: 1-276 < RES>
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        26-May-1995 #text_change 13-Aug-1999
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A;Title: Molecular characterization of a rat alpha-2B-adrenergic receptor. A;Reference number: A35642; MUID:90222177; PMID:2158103
A;Accession: A3542
A;Molecule type: mRNA
A;Residues: 1-453 <ZEN>
                                                                                                                                                                                                                                                       C;Superfamil
C;Keywords:
                                                                                                                                                                                                                                                                  A;Cross-references: GB:M32061; NID:g202589; A;Note: 169-Phe was also found C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha-2B-adrenergic receptor - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999 C;Accession: A35642
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A35642
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F;134-158/Domain: transmembrane #status predicted <TM4>
F;173-199/Domain: transmembrane #status predicted <TM5>
F;377-402/Domain: transmembrane #status predicted <TM6>
F;410-435/Domain: transmembrane #status predicted <TM7>
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A;Note: the authors translated the codon CCA for residue 161 as Phe, ACT R;Chruscinski, A.J.; Link, R.E.; Daunt, D.A.; Barsh, G.S.; Kobilka, B.K. Biochem. Biophys. Res. Commun. 186, 1280-1287, 1993.
A;Title: Cloning and expression of the mouse homolog of the human alpha?
A;Reference number: JH0693; MUID:92378586; PMID:1354956
A;Accession: JH0693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 6-228, 231-455 < CHR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Chen, W.M.; Chang, A.C.; Shie, B.J.; Chang, Y.H.; Chang, Blochim. Biophys. Acta 1171, 219-223, 1992
A;Title: Molecular cloning and characterization of a mouse A;Reference number: S28221; MUID:93129625; PMID:1336396
A;Accession: S28221
A;Status: preliminary
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Best Local
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  83
                                          78 WYF 80
                                                                   23 ATTFLILFTIFGNALVILAVLTSRSLRAPONLFLVSLAAADILVATLIIFFSLANELLGY 82
                                                                                          18 AITFLILFTIFGNALVILAVLTSRSLRAPONLFLVSLAAADILVATLIIPESLANBLLGY
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                                                                                                                                                                      63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 WCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALBYNSKRTPRRIKCIILTVWLIAAVI 143
                                                                                                                                                                                      Similarity
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85
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100.0%; Pr
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Pred. No.
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. 7.1e-53;
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nes 0;
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RESULT

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alpha-2B-adrenergic receptor - rat
c;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #seguence_revision 22-Jan-1993 #text_change 13-Aug-1999
C;Accession: A37869; S13023
R;Flordellis, C.S.; Handy, D.E.; Bresnahan, M.R.; Zannis, V.I.; Gavras, H.
Proc. Natl. Acad. Sci. U.S.A. 88, 1019-1023, 1991
A;Title: Cloning and expression of a rat brain alpha-2B-adrenergic receptor.
A;Reference number: A37869; MUID:91126047; PMID:1704126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Superfamily: vertebrate rnodopsin C; Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha-2-adrenergic receptor (clone RG10) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Dec-1991 #sequence_revision 03-Apr-1992 #text_change 13-Aug-1999
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R;Chang, Y.H.; Chang, N.C.; Chen, W.M.; Chang, A.C.
Biochem, Mol. Biol. Int. 29, 467-474, 1993

A;Title: Molecular characterization of a murine homologue
A;Reference number: A48392; MUID:93250567; PMID:8387367
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alpha 2C4 adrenoceptor subtype - mouse N/Alternate names: alpha 2C4 isoceptor N/Alternate mouse)
A;Crobs-references: GB:M58316; NID:g202585; PIDN:AAA40634.1; PID:g202586 A;Note: the authors translated the codon ACC for residue 69 as Asn and GR;Voigt, M.M.; MCCune, S.K.; Kanterman, R.Y.; Felder, C.C. FEBS Lett. 278, 45-50, 1991
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                                                                                         A; Molecule type: mRNA
A; Residues: 1-458 <FLO>
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C;Keywords: G protein-coupled receptor
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                                                                                                                                      Accession: A37869
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100.0%; Pred. No.
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                                            Asn and GCG for residue
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RESULT 10
A31237
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A;Residues: 1-39,'G',41-68,'N',70-154,'E',156-244,'S',246-458.<VOI>
A;Residues: 1-39,'G',41-68,'N',70-154,'E',156-244,'S',246-458.<VOI>
A;Cross-references: GB:X57659; NID:g288044; PIDN:CAA40861.1; PID:g288045
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane prote
                                                                                                                                                    C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 13-Aug-1999 (C;Accession: A31237; S14309; S14310 R;Regan, J.W.; Kobbilka, T.S.; Yang-Feng, T.L.; Caron, M.G.; Lefkowitz, R.J. Proc. Natl. Acad. Sci. U.S. A. 85, 6301-6305, 1988 A;Title: Cloning and expression of a human kidney cDNA for an alpha-2-adrend A;Reference number: A31237; MUID:88320430; PMID:2842764
R;Chhajlani, v.;
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A;Tille: Cloning of two mouse genes encoding alpha-2 adrenergic in antagonist binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alpha-2 adrenergic receptor - mouse
C;Species: Mus musculus (house mouse)
C;Datc: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
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  A;Cross-references: GB:J03853; NID:g178193; PIDN:AAA35513.1; PID:g178194 R;Chhajlani, V.; Rangel, N.; Uhlen, S.; Wikberg, J.E.S. FEBS Lett. 280, 241-244, 1991
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                                                                                  A;Molecule type: mRNA
A;Residues: 1-461 <REG>
                                                                                                                               A;Accession: A31237
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C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-458 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: I49480; MUID:92342131; PMID:1353249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: I49480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession:
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                                                                                                                                                                                                                                                                                                                 Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Status: preliminary; translated from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neurotransmitter receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VYLALDVLFCTSSIVHLCAISLDRYW 151
                                                                                                            mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Pred. No. 6.9e-17;
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                                                                                                                                                                                                                                    T.L.; Caron, M.G.; Lefkowitz, R.J.; Kobilka, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.9e-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 458;
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                                                                                                                                                                                       an alpha-2-adrenergic recepto:
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FEBS Lett. 280, 241-244, 1991 A;Title: Identification of an additional gene belonging A;Reference number: S14308; MUID:91192139; PMID:1849485

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the alpha(2) adrenergic

recep

A; Molecule type:

A; Accession: S14310

A;Residues:

95-223 <CH2>

GDB:ADRA2C; ADRARL2;

ADRA2L2; ADRA2RL2

A; Molecule type: DNA A; Residues: 95-223 < CHH>

A; Status: preliminary

A;Accession: S14309

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RESULT 13
B40392
                R; Lanier, S.M.;
                        alpha-2-adrenergic receptor (clone RG10) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Dec-1991 #sequence_revision 03-Apr-1992 #text_change
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                                                                                                                                                                                                                                                                                  A;Cross-references: GB:J05652; NID:g164303; PIDN:AAA30984.1; PID:g164304
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                    R;Guyer, C.A.; Horstman, D.A.; Wilson, A.L.; Clark, J.D.; Cragoe Jr., E.J.; Limbird, L.E J. Biol. Chem. 265, 17307-17317, 1990
A;Title: Cloning, sequencing, and expression of the gene encoding the porcine alpha-2-ad A;Reference number. A38316; MUID:91009167; PMID:2170371
A;Accession: A38316
                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-450 < GUY>
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
C;Accession: A38316
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A38316
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C;Superfamily: vertebrate rhodopsin
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R;Svensson, S.P.; Bailey, T.J.; Pepperl, D.J.; Grundstrom, N.; Ala-Uotila, S.;
Br. J. Pharmacol. 110, 54-60, 1933

A;Title: Cloning and expression of a fish a2-adrenoceptor.
A;Reference number: I50829; MUID:94035926; PMID:7693288

A;Accession: I50829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alpha 2-adrenoceptor - cuckoo wrasse
()Species: Labrus ossifagus (cuckoo wrasse)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 13-Aug-1999
C;Accession: I50829
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I50829
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Best Local !
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Best Local S
Matches 25
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Best Local (
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                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                          YLALDVLFCTSSIVHLCAISLDRYW 133
                                                                                                                                                                                  YLALDVLFCTSSIVHLCAISLDRYW 112
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   Downing, S.; Duzic,
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                                                                                                                                                                                                                                    Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative 0;
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Conservative 0; Mismatches
                                                                                                                                                                                                                                             5.6%; Score 25;
100.0%; Pred. No.
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100.0%; Pred. No. 6.2e-16;
ive 0; Mismatches 0;
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E.; Homcy, C.J
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                         13-Aug-1999
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A;Molecule type: DNA
A;Residues: 1-450 <FRA>
A;Residues: 1-650 <FRA>
A;Crose-references: GB:M23533; NID:g178195; PIDN:AAA51665.1; PID:g178196
R;Kobilka, B.K.; Matsui, H.; Kobilka, T.S.; Yang-Feng, T.L.; Francke, U.,
Science 238, 650-656, 1987
                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence revision 22-Jan-1993 #text_change C;Accession: A34169; A40132; S14311
R;Fraser, C.M.; Arakawa, S.; McCombie, W.R.; Venter, J.C.
J. Biol. Chem. 264, 11754-11761, 1989
A;Title: Cloning, sequence analysis, and permanent expression of cyclase attenuation and activation.
A;Reference number: A34169; MUID:89308571; PMID:2568356
A;Accession: A34169; MUID:89308571; PMID:2568356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alpha-2A-adrenergic receptor - human
N;Alternate names: alpha-2C10-adrenergic receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;106-131/Domain: hydrophobic <III>F;150-175/Domain: hydrophobic <HIV>F;159-218/Domain: hydrophobic <HDV>F;139-218/Domain: hydrophobic <HDV>F;375-400/Domain: hydrophobic <HVI>F;405-430/Domain: hydrophobic <VII>F;405-430/Domain: hydrophobic <VII>F;405-430/Domain: hydrophobic <VII>F;405-430/Domain: hydrophobic <VII>F;405-430/Domain: hydrophobic <VII>F;405-430/Domain: hydrophobic <VII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C/Superfamily: vertebrate rhodopsin C/Keywords: G protein-coupled receptor; F;34-99/Domain: hydrophobic <hDI>F;71-96/Domain: hydrophobic <hII>Fi71-96/Domain: hydrophobic <hIII>Fi71-96/Domain: hydrophobic <hIII-Fi71-96/Domain: hydrophobic <hIII-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: brain
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A; Residues: 1-450 < CHA>
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Mol. Cell. Biochem. 97, 161
A;Title: Molecular cloning,
A;Reference number: JH0190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha-2-adrenergic receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: JH0190
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JH0190
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C;Keywords: G protein-coupled receptor; transmembrane protein
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A;Molecule type: DNA
A;Residues: 1-450 <LAN>
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C;Superfamily: vertebrate rhodopsin
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A;Title: Isolation of rat genomic clones encoding subtypes of the alpha-2-adrenergic
A;Reference number: A40392; MUID:91244823; PMID:1645350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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and expression of the gene
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for the human platelet

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A,Reference number: A40132; MUID:88042789; PMID:2823383
A,Accession: A40132
A;Molecule type: DNA
A,Easidues: 1-103, T',105-156,'C',158-367,'L',369-450 <KOB>
A,Gross-references: GB:M18415; NID:g178191; PID:RAA,516421, PDID:g178192
A,Note: the authors translated the codon TGT for residue 157 as Val, and CTC for residue
A;Note: part of this sequence was confirmed by protein sequencing
R;Chhallani, V; Rangel, N; Uhlen, S; Wikberg, J.E.S.
PEBS Lett. 280, 241-244, 1991
A,Title: Identification of an additional gene belonging to the alpha(2) adrenergic recep
A;Reference number: $14311
A;Reference number: $14308; MUID:91192139; PMID:1849485
A;Accession: $14311
A;References: GGB:10538; OMIM:104210
A;Residues: 77-123,'P',125-209 <CHH>
C;Genetics:
A;Annote: percences: GGB:10538; OMIM:104210
A;Map position: 10425-10425
A;Introns: #Bteatue absent
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
C;Keywords: G protein-coupled receptor; transmemb
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Copyright
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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OM protein - protein search, using sw model

Run on: February 6, 2004, 18:19:31 ; Search time 10.0334 Seconds (without alignments) 2109.148 Million cell updates/sec

Perfect score: MDHQDPYSVQATAAIAAAIT.....QDFRRAFRRILCRPWTQTAW

US-09-692-077D-7

Title:

Scoring table: 0F1G0 Gapext 60.0

Gapop 60.0 ,

Word size : 20

Searched:

127863 ведв,

47026705 residues

Total number of hits satisfying chosen parameters:

30

Minimum Maximum D8 geq 9

length: 0 length: 2000000000

Database : Post-processing: Listing first 45 summaries SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
ַ	450	100.0	450	ᆄ	A2AB HUMAN	P18089 homo sapien
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11	63	14.	386	щ	A2AB_AMBHO	
12	63	14.	387	ب	A2AB_MACPR	v
13	63	14.0	453	٣	A2AB_RAT	8
14	62	13.	389	_	A2AB_PROHA	O19054 procavia ca
15	62	13.	392	μ	A2AB_BOVIN	077700 bos taurus
16	62	13.	397	<b>,_</b>	A2AB_TALEU	_
17	38	80	384	Н	A2AB_ECHTE	ω
18	26	5.	455	μ	A2AC_CAVPO	σ
19	26	5.8	458	_	A2AC_MOUSE	7
20	26	5.	458	Ъ	A2AC_RAT	P22086 rattus norv
21	26	5.	462	-	A2AC_HUMAN	U
22	26	5.	469	Н	A2AC_DIDMA	U
23	25	5.	432	Ь	A2AR_LABOS	_
24	25	5.	436	۲	A2AR_CARAU	_
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30	25		452	L	A2AA_BOVIN	Q28838 bos taurus

ALIGNMENTS

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RESULT 1
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91054503; PubMed=2173582; Chang A.C., Ho T.F., Chang N.-C.A.; "In vitro amplification by polymerase chain reaction of a partial "In vitro amplification by polymerase chain reaction of a partial "In vitro amplification by polymerase chain reaction of a partial "In vitro amplification by polymerase chain reaction of a partial "In vitro amplification by polymerase chain reaction of a partial "In vitro amplification by polymerase chain reaction of a partial "In vitro amplification by polymerase chain reaction of a partial "In vitro amplification by polymerase chain reaction of a partial "In vitro amplification by polymerase chain reaction of a partial "In vitro amplification by polymerase chain reaction of a partial "In vitro amplification by polymerase chain reaction of a partial "In vitro amplification by polymerase chain reaction of a partial "In vitro amplification by polymerase chain reaction of a partial "In vitro amplification by polymerase chain reaction of a partial "In vitro amplification by polymerase chain reaction of a partial "In vitro amplification by polymerase chain reaction of a partial "In vitro amplification" of a partial "In vitro amplification" of a partial "In vitro amplification" of a partial "In vitro amplification" of a partial "In vitro amplification" of a partial "In vitro amplification" of a partial "In vitro amplification" of a partial "In vitro amplification" of a partial "In vitro amplification" of a partial "In vitro amplification" of a partial "In vitro amplification" of a partial "In vitro amplification" of a partial "In vitro amplification" of a partial "In vitro amplification" of a partial "In vitro amplification" of a partial "In vitro amplification" of a partial "In vitro amplification" of a partial "In vitro amplification" of a partial "In vitro amplification" of a partial "In vitro amplification" of a partial "In vitro amplification" of a partial "In vitro amplification" of a partial "In vitro amplification" of a partial "In vitro amplification" of a partial "In vitr
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Small K.M., Brown K.M., Forbes S.L., Liggett S.B.;
Small K.M., Brown K.M., Forbes Hutracellular acidic residues of the
"Polymorphic deletion of three intracellular acidic residues of the
alpha 2B-adrenergic receptor decreases G protein-coupled receptor
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Submitted (JUL-1997)
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01-NOV-1990 (Rel. 16, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
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Branchek T.A., Hartig
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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J. Biol. Chem. 276:4917-4922(2001).
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Weinshank R.L., Zgombick J.M., Macchi M.,
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THEM. BIOPHYS. Res. COMMUN. 172:817-823 (1990).
FUNCTION: ALPHA-2 ADRENBERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-FUNCTION: ALPHA-2 ADRENBERGIC RECEPTORS MEDIATE THE ACTION OF GINDUCED INHIBITION OF ADAVILATE CYCLASE THROUGH THE ACTION OF GPOTENCY FOR AGONISTS OF THIS RECEPTOR PROTEINS. THE RANK ORDER OF POTENCY FOR AGONISTS OF THIS RECEPTOR
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M34041;
M38742;
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AAA62823.1;
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420 360

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R GO; GO:0005887; C:integral to plasma membrane; TAS.

R GO; GO:0004938; F:alpha2-adrenergic receptor activity; TAS.

R GO; GO:0007267; F:cell-cell signaling; TAS.

R GO; GO:0007267; F:cell-cell signaling; TAS.

R GO; GO:000726; P:cell-cell signaling; TAS.

R FAINTS; PR00207; Trn I; I.

DR PAINTS; PR00207; Trn I; I.

R PROSITE; PS00237; G PROTEIN_RECEP_F1_2; 1.

KW G-protein coupled receptor; Transmembrane; Multigene family;
R PROSITE; PS0023; G PROTEIN_RECEP_F1_2; 1.

KW G-protein coupled receptor; Transmembrane; Multigene family;
R PROSITE; PS0023; G PROTEIN_RECEP_F1_2; 1.

EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 39 49 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 39 49 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 50 75 2 (POTENTIAL).

FT TRANSMEM 50 75 2 (POTENTIAL).
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EMBL; AF005900; AAB62558.1; -
FIR; A37223; A37223;
HSSP; P29274; 1MMH.
Genew; HGNC:282; ADRAZB.
MLM; 104260; -
GO; GO:0005887; C:integral to
GO; GO:0004938; F:alpha2-adrer
GO; GO:0007267; P:cell cell si
                                                                                                                     AŚAREVNGHŚKŚTGEKEEGETPEDTGTRALPPŚWAALPNSGQGQKEG
                                                                         ASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGGGGKEGVCGASPEDEAEEE
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Llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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IMPLICATED IN CATECHOL AGONIST BINDING
(BY SIMILARITY).

IMPLICATED IN CATECHOL AGONIST BINDING
(BY SIMILARITY).

(BY SIMILARITY).

MISSING (COMMON POLYMORPHISM; FREQUENCY
IN CAUCASIANS 0.12 AND IN AFRICAN-
AMERICANS 0.12; IMPAIRED PHOSPHORYLATION
AND DESENSITIZATION BY GRKS).

/FIId=VAR 0.14958.

QL -> HV (IN REF. 1 AND 2).
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ASP/GLU-RICH (ACIDIC).
BY SIMILARITY.
PALMITATE (POTENTIAL).
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IMPLICATED IN LIGAND BINDING
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7 (POTENTIAL)
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PROSITE; PS00237; G_PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G_PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Transmembrane; Multigene family;
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                                                                                                                                                                                                                                                                                                      Phosphorylation; Lipoprotein;
NON TER 1 1 1
TRANSMEM <1 25
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HSSP; P29274; 1MMH.
Interpro; IPR000276; GPCR_Rhodpsn.
Pfam; PF000001; 7tm 1; 1.
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Springer M.S., Cleven G.C., Madsen O.J., de Jong W.W., Waddell V.G.,
Amerine H.M., Stanhope M.J.;
"Endemic African mammals shake the phylogenetic tree.";
Nature 388:61-64(1997).
-i- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
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019012;
15-JUL-1998
15-JUL-1998
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Erinaceus europaeus (Western European hedgehog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Insectivora, Erinaceidae, Erinaceinae, Erinaceus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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7 (POTENTIAL).
BY SIMILARITY.
ASP/GLU-RICH (ACIDIC).
IMPLICATED IN LIGAND BINDING
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CYTOPLASMIC (P
4 (POTENTIAL).
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                                                                                                                                                                                               (POTENTIAL).
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15-JUL-1998
15-JUL-1998
28-FEB-2003
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                   G-protein coupled
Phosphorylation,
NON TER 1
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                                                             Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRTHODOPSN.

PROSTTE; PS00237; GPROTEIN RECEP F1 1; 1.

PROSITE; PS50262; GPROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=97357151; PubMed=9214502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Tubulidentata; Orycteropodidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Orycteropus
                                                                                                                                                                               InterPro, IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                EMBL; Y12522; CAA73122.2; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                   between
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15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
                                                                                                                                                                                                                                                                                            ween the Swiss Institute of Bioinformatics and the Emph Outer Buropean Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is not profit institutions as long as its content is in the statement is not removed. Usage by and for complete and this statement is not removed. Usage by and for complete and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE
                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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EMBL; Y15946; CAA75899.2;
                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                               between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
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(Rel. 41, Last annotation update)
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HSSP; P29274;

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RESULT 5
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                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no waentities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
            EMBL; Y12525; CAA73125.1; -. HSSP; P29274; IMMH.
                                                                                                                                            Springer M.S. Cleven G.C., Madsen O.J., de Jong W.W., Marine H.M., Stanhope M.J.;

"Endemic African mammals shake the phylogenetic tree.";

Nature 388:61-64(1997).

-!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE (
INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE
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SEQUENCE FROM N.A.
MEDLINE=97357151; PubMed=9214502;
MEDLINE=97357151; PubMed=9214502;
Medline=97357151; Madse
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Mammalia; Eutheria;
NCBI_TaxID=9783;
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PROSITE; PS50262; G_PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
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SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
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4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

BY SIMILARITY.

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RAGBER O.J.,

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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-

-!- FUNCTION: INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
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MEDLINE=98334573; PubMed=9667998;
Madsen O.J., Waddell V.G.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

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renergic receptor (Alpha-2B adrenoceptor) (Fragment).
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16-OCT-2001
28-FEB-2003
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SEQUENCE FROM N.A.
Stanhope M.J., Madsen
Springer M.S., Madsen
Submitted (NOV-1999) t
                                                           Dugong dugon (Dugong).
Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Si
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Multigene family.

NON_TER 1 1
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Pfam; PF00001; 7tm_1; 1.
                                                  NCBI_TaxID=29137;
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Best Local :
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01-NOV-1997
16-OCT-2001
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STRAIN=Hartley;
MEDLINE=96152573; PubMed=8573196;
Svensson S.P., Bailey T.J., Porter A.C., Richman J.G., F
"Heterologous expression of the cloned guinea pig alpha
and alpha 2C adrenoceptor subtypes. Radioligand binding
                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10141;
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Eukaryota; Metazoa; Chordata;
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01-NOV-1997 (Rel. 35, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Alpha-2B adrenergic receptor (Alpha-2B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P29274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEINS.
-!- SUBCELLULAR LOCATION:
-!- SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000276; GPCR_Rhodpsn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                         CAVPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 NSKRTPRRIKCIILTVWLIAA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00001; 7tm 1; 1.
S; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y15947; CAA75900.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NSKRTPRRIKCIILTVWLIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     390 AA;
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26
37
63
73
73
118
118
1181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor;
                                                                                                                                                                             Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

ASP/GLU-RICH (ACIDIC).

BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 81;
Pred. No
                                                                                                                                                                                                                                                                   (Alpha-2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR
3 (POTENTIAL)
                                                                                                                                                                           Hystricognathi;
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2 (POTENTIA
                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     779F849267F9F314 CRC64;
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                                                                                                                                                                                                                                                               update)

adrenoceptor).
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                                                                                                                                                                             Caviidae; Cavia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 390;
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                                               Regan
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RESULT 9
A2AB MOUSE
ID A2AB MOUSE
AC P30545;
DT 01-APR-1993 (
DT 01-APR-1993 (
DT 16-OCT-2001 (
DE Alpha-2B adre
a GN ADRA2B.
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Best Local &
                                  Alpha-2B adrenergic
ADRA2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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LIPID
DOMAIN
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TRANSMEM
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; #292/7; Zrau...
InterPro; IPRO0276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1. —
PRINTS; PR0023; GPCRHODOPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane;
Phosphorylation; Lipoprotein; Palnitate.
Phosphorylation; Lipoprotein; Palnitate.
PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             functional coupling to a CAMP-responsive reporter gene.";
Biochem. Pharmacol. 51:291-300(1996).

-i- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G.

-i- SUBCELIULAR LOCATION: Integral membrane protein.

-i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                               142
                                                                                                                                                                                                                                                                142
                                                                                                                                                                                                                                                                                                  82
                                                                                                                                                                                                                                                                                                                                   82
                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                    VISLPPLIYKGDQGP 156
                                                                                                                                                                                                                                             VISLPPLIYKGDQGP 156
                                                                                                                                                                                                                                                                       RTWCEVYLALDVLECTSSIVHLCAISLDRYWAVSRALEYNSKRTPRRIKCIILTVWLIAA 141
                                                                                                                                                                                                                                                                                                  RTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTPRRIKCIILTVWLIAA
                                                   (Rel. 25, Created)
(Rel. 25, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                      448 AA;
                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                 STANDARD;
                                receptor (Alpha-2B adrenoceptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38
49
75
108
130
153
168
192
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394
403
427
448
163
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                                                                                                                                                                                                                                                                                                                                                                                                                                    49597 MW;
                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                     16.7%;
                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                             Score 75;
Pred. No.
                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                        IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (POTENTIAL).
CYTOPLASMIC (P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PALMITATE (POTENTIAL).
ASP/GLU-RICH (ACIDIC).
IMPLICATED IN LIGAND BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (
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3 (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY
                                                                                                                              455
                                                                                                                                                                                                                                                                                                                         DB 1; 10. 2e-51; Indels
                                                                                                                            A
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                                                                                                                                                                                                                                                                                                                                                                                    Length 448;
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                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                            141
 SITE
CONFLICT
                                                                                                                                         DISULFID
LIPID
                                                                      SITE
                                                                                                       DOMAIN
SITE
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TRANSMEM
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Pfam; PF00001; 7tm 1; 1.

PRANTS; PR00237; GECRHODDPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1 1; 1.

PROSITE; PS00237; G_PROTEIN_RECEP_F1 2; 1.

G-PROSETE; PS50262; G_PROTEIN_RECEP_F1 2; 1.

G-PROTECAIN_COUPLed receptor; Transmembrane;

Phosphorylation; Lipoprotein; Palmitate.

Phosphorylation; Lipoprotein; Palmitate.

PMOMAIN 1 17 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:87935; Adra2b.
GO; GO:0004938; F:alpha2-adrenergic receptor activity; IDA.
GO; GO:0001525; P:mapKKK cascade; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adrenergic receptor.",
Biochem, Biophys. Res. Commun. 186:1280-1287(1992).
-i- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S28221; S28221.
HSSP; P29274; 1MMH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M94583; AAA73895.1;
EMBL; L00979; AAA37131.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92378586; PubMed=1354956; Chruscinski A.J., Link R.E., Daunt D. "Cloning and expression of the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-93129625; PubMed-1336396; Chen W.-M., Chang A.C., Shie B.J., Chang Y.-H., Chang N.-C.A.; "Molecular cloning and characterization of a mouse alpha 2C2 adrenoceptor subtype gene."; Biochim. Biophys. Acta 1171:219-223(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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STRAIN=DBA/2; TISSUE=Liver;
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                                185
                                                                181
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54
80
90
113
135
158
174
198
377
401
410
434
455
169
316
                            185
   SIMILARITY).

IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).

IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
                                                                                  PALMITATE (POTENTIAL).
ASP/GLU-RICH (ACIDIC).
IMPLICATED IN LIGAND BINDING
                                                                                                                                             BY SIMILARITY.
                                                                                                                                                                          EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL)
                                                                                                                                                                                                                CYTOPLASMIC
6 (POTENTIAL)
                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL)
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CYTOPLASMIC (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                        (POTENTIAL).
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alpha 2-c2
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a collaboration MRL outstation -

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A2AB_DIDMA
077715;
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15-JUL-1999 (Rel. 38,
16-OCT-2001 (Rel. 40,
Alpha-2B adrenergic 1
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TRANSMEM
                                                                                                                                                        PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=98334573; Publ
Stanhope M.J., Madben
Springer M.S.;
                                                                                                                                                 G-protein
NON_TER
                                                                                                                                                                                                       HSSP; P29274; 1MMH.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                             the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                         between
                      TRANSMEM
                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                          "Highly congruent molecular support for a of endemic African mammals.";
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                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                     . Phylogenet. Evol. 9:501-508(1998).
FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
                                                                                                                                                                                                                                                                                                                                                                                PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                           INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH
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                                                                                                                                                                                           PR00237; GPCRRHODOPSN
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38, Last sequence update)
40, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=9667998;
dsen O.J., Waddell V.G.,
230

    Last annotation update)
    receptor (Alpha-2B adrenoceptor) (Fragment).

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                                                                                       1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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; A3954AD76E0E6263 CRC64;
                                                                              CYTOPLASMIC
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RESULT 11
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Best Local
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16-OCT-2001
28-FEB-2003
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MEDLINE=97357151; PubMed=9214502;
MEDLINE=97357151; Cleven G.C., Madse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMBHO
                                                                                                                                                                     EMBL; Y12526; CAA73126.2; -.
HSSP; P29274; 1MMH.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                        Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
                                                                                                                                                                                                                                                                                                                                                                                                                                           Springer M.S., Cleven G.C.,
Amrine H.M., Stanhope M.J.,
"Endemic African mammals sh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A2AB_AMBHO
018935;
                                                                                    Phosphorylation;
NON_TER 1
                                                                                                         PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein_coupled_receptor; Transmembrane;
                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Cra
Mammalia; Eutheria; Insectivora;
                                                                         TRANSMEM
                                                                                                                                              PRINTS; PR00237; GPCRRHODOPSN
                                                                                                                                                            Pfam; PF00001; 7tm
                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                             Madsen
                                                                                                                                                                                                                                                                                                                                                                                                         REVISION TO 121.
                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 388:61-64(1997).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amblysomus hottentotus (Hottentot golden mole).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alpha-2B adrenergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADRA2B
                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                PROTEINS
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271
382
382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 36, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
(Rel. 41, Faceptor (Alpha-2B adrenoceptor) (Fragment).
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37
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283
382
41870
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                                                                                                                                                                                                                                                                                                                                                                                                                                             shake the phylogenetic tree.";
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
ASP/GLU-RICH (ACIDIC).
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                                                                                                           Multigene family;
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Amblysomus.
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Matches 63
       EMBL; Y12524; CAA73124.2;
HSSP; P29274; IMMH.
InterPro; IPR000276; GPCR Rhodpsn.
                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                          Springer M.S., Cleven G.C., Madsen O., de Jong W.W., Wad
Amrine H.M., Stanhope M.J.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE C
INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE
                                                     entitles requires a license agreement (some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                           Macroscelides proboscideus (Short-eared elephant shrew).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Macroscelidea; Macroscelididae; Macroscelides.
                                                                             modified
                                                                                                                                                                                                                                                "Endemic African mammal Nature 388:61-64(1997). [2]
                                                                                                                                                                                                                                                                   MEDLINE-97357151; PubMed-9214502;
Springer M.S., Cleven G.C., Madsen
Amrine H.M., Stanhope M.J.;
"Endemic African mammals shake the
                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                      019025;
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                                                                                                                                        SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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                                                                           non-profit institutions as long and this statement is not removed.
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Pred. No.
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EXTRACELLULAR (POTENTIAL)

7 (POTENTIAL)
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IMPLICATED IN CATECHOL AGONIST BINDING
(BY SIMILARITY).
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                                                                                                                                                                                                                                                                   phylogenetic tree
                                                                                                                                                                                                                                                                                                                                                                                                                                                 387
                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                       de Jong W.W., Waddell V.G
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Best Local :
            MEDLINE=95275492; PubMed=7755946;
le JOSSEC M., Cloix J.F., Pecquery R., Giudicelli Y.,
"Differential sodium regulation between salt-sensitive
resistant Sabra rats is not due to any mutation in the
2B-adrenoceptor gene.";
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P19328; Q63021;
01-NOV-1990 (Rel. 16, Created)
16-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update).
Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor)
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"Molecular characterization
"Acad Sci. U.S.,
                                                                                                                                                                                                                  Zeng D., Harrison Lu Z., Lynch K.R.;
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MEDLINE=90222177;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
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PROSITE; PS00237; GPCOTEIN RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein_coupled_receptor; Transmembrane;
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                                                                                                                   TISSUE=Kidney;
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                                                                                                                                                                                                                                       PubMed=2158103;
J.K., D'Angelo
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                                                                                                                                                                            ation of a rat alpha 2B-adrenergic receptor."; U.S.A. 87:3102-3106(1990).
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IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).

IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
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                                                    salt-sensitive
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Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00001; 7tm 1; 1.

PRINTS; PR000237; GPCRRHODDPSN.

PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein_coupled_receptor; Transmembrane; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                         A2AB_PROHA
019054;
                                           PROHA
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PIR; A35642; A35642.
                                                                                                                                                                                                                                                                                              TRANSMEM
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                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                     GIGIT
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SIMILARITY: BELONGS TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M32061; AAA40635.1; -. X74400; CAA52411.1; -.
                                                                            83
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                                                                             WYF 85
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162
453
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(Rel.
(Rel.
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43
81
91
114
136
175
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                                 STANDARD;
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36, Created)
36, Last sequence update)
40, Last annotation update)
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54
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375
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169
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                                                                                                                                                       14.0%;
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TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                 MW;
                                                                                                                                               0
                                                                                                                                                       Score 63;
Pred. No.
                                                                                                                                                                                                                                                            BY SIMILARITY.
PALMITATE (POTENTIAL).
ASP/GLU-RICH (ACIDIC).
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2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL).
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BY SIMILARITY
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6 (POTENTIA)
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5 (POTENTIAL).
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7 (POTENTIAL).
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                                                                                                                                                                                (BY SIMILARITY).
C -> R (IN REF. 2).
DA -> EP (IN REF. 2).
BCA040FFF9A310EB CRC64;
                                                                                                                                                                                                                  (BY SIMILARITY).
IMPLICATED IN CATECHOL
                                                                                                                                                                                                                                                    IMPLICATED
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                                 PRT;
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Query Match
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=97357151; PubMed=9214502;
Springer M.S., Cleven G.C., Madsen O.J., de Jong W.W., 1
Amrine H.M., Stanhope M.J.;
"Endemic African mammals shake the phylogenetic tree.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00237; G_PROTEIN_RECEP_F1 1; 1. PROSITE; PS50262; G_PROTEIN_RECEP_F1 2; 1. G-protein coupled receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Y12523; CAA73123.1; -. HSSP; P29274; 1MMH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Procavia capensis habessinica (Abyssinian hyrax).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Bu
Mammalia; Eutheria; Hyracoidea; Procaviidae; Procavia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00237; GPCRRHODOPSN
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ADRA2B.
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INDUCED INHIBITION
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                                                                                                                                                                               MW;
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O FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                    0;
                                                                                                                    Score 62; DB; Pred. No. 2.7
                                                                                                                                                                                                                           IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
IMPLICATED IN CATECHOL AGONIST BINDING
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BY SIMILARITY
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                                                                                                                                  DB 1; Le
2.7e-41;
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67

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RESULT 15
A2AB BOVIN STANDARD; PRT; 392 AA.

ID A2AB BOVIN STANDARD; PRT; 392 AA.

AC 077700;
DT 15-JUL-1999 (Rel. 38, Created)
DT 6-CCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
                                                                                                                                     Query Match
Best Local Similarity
Matches 62; Conserv
                                                     NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                             G-protein
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DOMAIN
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                                                                                              SITE
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DOMAIN
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PRINTS; PR00237; GFCRHODOPSN.

PROSITE; PS00237; G PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G_protein coupled receptor; Transmembrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98334573; PubMed=9667998; Stanhope M.J., Madsen O.J., Waddell V.G., Springer M.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Y15944; CAA75897.2; -. HSSP; P29274; 1MMH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Highly congruent molecular support for a diverse superordinal clade of endemic African mammals.";
                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                          NIAMOC
                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane protein (By similarity). SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Phylogenet. Evol. 9:501-508(1998).
FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
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13.8%; Score 62; DB llarity 100.0%; Pred. No. 2. Conservative 0; Mismatches
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EXTRACELLULAR (POTENTIAL)
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SIMILARITY).
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EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                           BY SIMILARITY.
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              DB 1; Length 392;
2.7e-41;
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Search completed: February 6, 2004, 18:24:04 Job time : 11.0334 secs

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Perfect score:
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Q8k373 polodontia
Q9g120 cynopterus
Q8g78 chinchilla
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Matches 192;
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PROSITE; PS00237; G PROTEIN RECEP F1 2; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Receptor; Transmembrane.
                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; AJ251187; CAC16698.1; -
InterPro; IPR000276; GPCR Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                      SEQÜENCE
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Madsen O., Scally M., Douady C., Kao D., DeBry R., Adkins R.,
Amrine H., Stanhope M., de Jong W., Springer M.;
"Parallel adaptive radiations in two major clades of placental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tupaia tana (Large tree shrew).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Scandentia; Tupaidae; Tupaia.
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389 AA;
42.7%; Score 192; DE ilarity 100.0%; Pred. No. 3.7 Conservative 0; Mismatches
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                                                                                                 42631 MW; A9DC6F864487A2BE CRC64;
                    Score 192; DB 6; Le
Pred. No. 3.7e-178;
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19 ITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADILVATLIIPFSLANELLGYW 78

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Felis silvestris catus (Cat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Wannalla; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                    Q9GL17, PRELIMINARY, PRT, 387 AA.
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
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Feating advenergic receptor 2B (Fragment).
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Ol-MAR-2003 (TrEMBLrel. 23, Created)
Ol-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Tupha-2B adrenceptor. 23, Last annotation update)
Eukaryota, Metasoa; Chordataree shrew).
NCBI [TaxID=37347]; Scandentia, Tupaiidae; Tupaia. Euteleostomi;
[1] [TaxID=37347];
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19 ITELLETIFGNALVILAVLTSRSLRAPONLELVSLAAADILVATLIIPESLANELLGYW 78
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al Similarity 42.2%; Score 190; DB 6;
190; Conservative 0; Mismatches 0
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66 YFRRIMCEVYLALDVLFCISSIVHLCAISLDRYWAVSRALEYNSKRIPRRIKCIILITVWL 138
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RA Teeling E.C., Madden O., Van Den Bussche R.A., de Jong W.W.,
Stanhope M.J., Springer M.S.,
RT "Microbat paraphyly and the convergent evolution of a key innovation
DR E.C., Mallar LOCATION: INTEGRAL MEMBRANE PROTEIN (By Innovation
RI Proc. INSTITUTARE SOCIETY: BELONGS TO FAMILY 1 OF G-PROTEIN (By SIMILARITY)
DR Pfam, D. 1985, GPOTEIN RECEPFI J.
DR PROSITE; PS0021, J.D., RANGLASH.
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REGULTS: PS0021, J.D., RANGLASH.
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DT 01-UUN-2002 (TrENBLrel. 21, Created)

DT 01-WR-2003 (TrENBLrel. 21, Last sequence update)

E Alpha 2B adrenergic receptor (Fragmention update)

ANRA2B. (Common tube-nosed fruit bat).
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Rukaryota; Metazoa; Chordata; Ctaniata; Vertebrata; Euteleostomi;
Phermodinae. Nychimene Optera; Megachiroptera; Pteropodidae;
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Matches 184; Conservative 0; Mismatches 0; Indels
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6 ITELILETIEGNALVILAVLTSRSLRAPONLELVSLAAADILVATLIIPESLANELLGYW 78
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Madsen O., Scally M., Douady C., Kao D., DeBry R., Parallel, Stanhope M., de Jong W., Springer M., Adkins R.,
mammals ", dadptive radiations in two major clades of placental
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; 42907 MW, C203401584C560EE CRC64,
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01-OCT-2002
01-MAR-2003
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SEQUENCE
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Molecular evolution of the alpha 2B adrenergic receptor.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ505819; CAD44320.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PP00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hylomys suillus (short-tailed gymnure).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Insectivora; Erinaceidae; Hylomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=48897;
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186
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002 (TrEMBLrel. 22, Last sequence update)
003 (TrEMBLrel. 23, Last annotation update)
adrenergic receptor (Fragment).
                                                                                                                                                                                                                              YFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALBYNSKRTPRRIKCIILTVWL
                                                                                                                                                                                                                                                                                                                              ITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAPADILVATLIIPFSLANELLGYW 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKRS 189
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391 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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189
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43133 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                            40.9%; Score 184; DB 6; Length 391; 100.0%; Pred. No. 2.3e-170;
                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EB55AAD36B8A9769 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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2.3e-170;
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Best Local S
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01-MAR-2001
01-OCT-2002
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NON_TER
NON_TER
SEQUENCE
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SEQUENCE FROM N.A.

Wadsen O., Willemsen D., Ursing B.M., Arnason U., de Jong W

Molecular evolution of the alpha 2B adrenergic receptor.";

Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ505820; CAD44321.1;

InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9GL18;
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Q8MIDO;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                              SEQUENCE FROM N.A.
MEDLINE=21082081; PubMed=11214318;
Madsen O., Scally M., Douady C., Kao
Amrine H., Stanhope M., de Jong W., S
"Parallel adaptive radiations in two
                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9805;
                                                                                                                                                                                                                                                                                 Diceros bicornis (Black rhinoceros).
Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Perissodactyla; Rhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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Eukaryota; Metazoa; Chordata; Craniata; Verteb
Mammalia; Eutheria; Pholidota; Manidae; Manis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alpha 2B adrenergic receptor ADRA2B.
-!- SUBCELLULAR LOCATION:
-!- SIMILARITY: BELONGS T
EMBL; AJ251184; CAC16686.
                                                                     Nature 409:610-614(2001).
                                                                                             mammals.";
                                                                                                                                                                                                                                                                                                                                                                               Alpha adrenergic
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                                                                                                                                                                                                                                                                                                                                                                             (TTRMBLrel. 16, Created)
(TTRMBLrel. 16, Last sequence update)
(TTRMBLrel. 22, Last annotation updat
argic receptor 2B (Fragment).
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399
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BELONGS TO :
CAC16686.1;
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399
; 43888 MW;
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                   INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
PAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 184; |
; Pred. No. 2
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, Springer M.;
wo major clades
                                                                                                                                                                                                                                                                                      Rhinocerotidae;
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Diceros.
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SO FT CR

Query Match Best Local Simi Matches 171;

Similarity

Conservative

SEQUENCE

388 AA;

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"Resolution of the early placental mammal radiation usi phylogenetics."; Science 294:2348-2351(2001). RMBL, AJ315939; CAC87003.1; -. RILEPPIO; IPR000276; GPCR_Rhodpsn. RP60001; 7tm 1; 1. RPINTS: PR000237; GPCRHODDPSN. RPINTS: PR00237; GPCRHODDPSN. RPROSITE; PS00237; GPROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE=21608557; PubMed=11743200;

Murphy W.J., Eizirik E., O'Brien S.J., Madsen

Douady C.J., Teeling E., Ryder O.A., Stanhope

Springer M.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tapirus terrestris (Lowland tapir) (Brazilian tapir).
Bukaryota, Metazoa, Chordata, Craniata, Verrebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Tapiridae, Tapirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00001; /Lm_i, PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Receptor; Transmembrane.
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                      IAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASS 177
                                                                     YFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTFRRIKCIILTVWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTPRRIKCIILTVWL
                                                                                                             ITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADILVATLIIFFSLANELLGYW 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ĠĎQĠPQPRĠŖPQĊĸĹŃQĖÁWYIĹASSĪĠŚPFĀPĊĹĬMĬĹVYĹŖĨŶĹĨAKŔŚ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ĹVĬĹAVĹŤŚRŚĹŔAPQNĹFĹVŚĹAAADĬĹVÁŤĹĬĬPFŚĿANEĹĹĠŶŴŶFRRTWCEVYĽAĹ
                                                                                                                                                                                   35.3%; Score 159; DB 6;
llarity 100.0%; Pred. No. 5.3e-14
Conservative 0; Mismatches 0
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100.0%; Pre
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          RESULT 10
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A Huchon D., Madsen O., Sibbald M.J.J.B., Ament K., Stanhope M.,

A Catzeflls F., de Jong W.W., Douzery E.J.P.;

T "Rodent phylogeny and a timescale for the evolution of Glires:

"T evidence from an extensive taxon sampling using three nuclear gene

L Mol. Biol. Evol. 0:0-0(2002).

ENBL; A.4427255; CAD20293.; -

DR InterPro; IPR000276; GPCR Rhodpsn.

PRAINTS; PR00237; GPCRRHODDSN.

PRAINTS; PR00237; GPCRRHODDSN.

PRAINTS; PR00237; GPCRHODDSN.

DR PROSITE; PS00237; GPCRHODDSN.
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Q8K1U3
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SEQUENCE FROM N.A.

MEDLINE=21608557; PubMed=11743200;

Murphy W.J., Eizirik E., O'Brien S.J., Madsen

Douady C.J., Teeling E., Ryder O.A., Stanhope

Springer M.S.;
                                                                                                                                                                                   Q8K4Y3; PRELIMINARY; PRT; 392 AA.
Q8K4Y3; O1-OCT-2002 (TrEMBLrel. 22, Created)
O1-OCT-2002 (TrEMBLrel. 22, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Alpha 2B adrenergic receptor (Fragment).
                                                                                                                             Sciurus vulgaris (Red squirrel).
Eukaryota; Metazoa; Chordata; Cr.
Mammalia; Eutheria; Rodentia; Sc
                                                                                               NCBI_TaxID=55149;
                                                                                                                          Sciurus
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Q8K1U3;
01-OCT-2002
01-OCT-2002
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9995;
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01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
Alpha 2B adrenergic receptor
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392
; 42811 MW;
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100.0%; Pred. No. 2.2e-132;
tive 0; Mismatches 0;
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Sciurognathi;
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Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                      Vertebrata; Euteleostomi;
thi; Sciuridae; Sciurinae;
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Q8MK45; Q8MK45

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EMBL; Ay427256; CD120294.1; -.

InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GFORRHOODESN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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01-OCT-2002 (TYEMBLYE1. 22, Last sequence update)
01-MAR-2003 (TYEMBLYE1. 23, Last annotation updat
Alpha 2B adrenergic receptor (Fragment).
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Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00231; GPCRRHODDPSN.

PROSITE; PS00237; G PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Aplodontidae; Aplodontia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aplodontia rufa (Mountain beaver).
Eukaryota; Metazoa; Chordata; Cran
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Science 294:2348-2351(2001).
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01-MAR-2001
01-MAR-2001
01-OCT-2002
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PROSITE; PS00237; GPROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Receptor; Transmembrane.

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SEQUENCE 383 AA; 41945 MW: Cliencon Coupled Coupled Cliency Coupled Cliency Coupled Cliency Coupled Cliency Coupled Cliency Coupled Cliency Coupled Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cliency Cl
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MEDLINE=21082081; PubMed=11214318;

MEDLINE=21082081; PubMed=11214318;

Maddsen O., Scally M., Douady C., Kao D., DeBry R.,

Amrine H., Stanhope M., de Jong W., Springer M.;

"Parallel adaptive radiations in two major clades
                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                           Phoca vitulina (Harbor seal).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation updat
Alpha adrenergic receptor 2B (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9GL07
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EMBL; AJ251181; CAC16684.1;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;
Pteropodinae; Cynopterus.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation updat
   SEQUENCE FROM N.A.
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Local Similarity 100.0%;
hes 140; Conservative
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Protein COUPLED RECEPTORS.
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; Pred. No. 1.6e-127;
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                                                                                                     Craniata; Vertebrata; ; Pinnipedia; Phocidae;
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Catzeflis F., de Jong W.W., Douzery E.J.P.;
"Rodent phylogeny and a timescale for the evolution
evidence from an extensive taxon sampling using the
Mol. Biol. Evol. 0:0-0(2002)
Mol. Biol. Evol. 0:0-0(2002)
EMBL; AJ477252; CAD20290.1; -
InterPro. IPR000276; GPCR_Rhodpsn.
PRINTS; PR00031; Ttm 1; 1.
PRINTS; PR00237; GFCRRHODDPSN.
PROSITE; PS00237; GFCRRHODDPSN.
PROSITE; PS00237; GFCRRHODDPSN.
PROSITE; PS00237; GFCRRHODDPSN.
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Q8KIW8;
Q8KIW8;
Q1-OCT-2002 (TrEMBLrel. 22, Created)
Q1-OCT-2002 (TrEMBLrel. 22, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Q1-MAR-2003 (Tremblizel. 23, Last annotation update)
                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bathyergus suillus (Cape dune mole-rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Bathyergidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=#5234';
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Nature 409:610-614(2001).

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

INTERPOS IPRO00276; GPCR Rhodpsn.

Pfam; PF00001; 7tm 1, 1.

PRINTS; PR00237; GFCRHODOPSN.

PROSITE; PS00237; GPROTEIN_RECEP_F1 1; 1.

PROSITE; PS00237; G_PROTEIN_RECEP_F1 2; 1.

G-PROTEIS: PS00237; G_PROTEIN_RECEP_F1 3; 1.

G-PROTEIS: PS00237; GPROTEIN_RECEP_F1 3; 1.

G-PROTEIS: PS00237; GPROTEIN_RECEP_F1 3; 1.
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Madsen O., Scally M., Douady C., Kao D., DeBry R., Adkins R.,
Amrine H., Stanhope M., de Jong W., Springer M.;
"Parallel adaptive radiations in two major clades of placental
                         140;
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100.0%; Pred. No. 1.6e-127;
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tive 0; Mismatches 0;
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Search completed: February Job time : 34.1104 secs

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RESULT 15
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"Rodent phylogeny and a timescale for the evolution of Glires: evidence from an extensive taxon sampling using three nuclear genes.", Mol. Evol. 0:0-0(2002).
EMBL; AJ427271; CAD20309.1; -.
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Q8CG78;
Q1-MAR-2003
01-MAR-2003
01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Alpha 2B adrenergic receptor (Fragment).
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ÍAAVISLÞÞLÍÝKGDQGÞQÞ
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100.0%; Fi
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Post-processing: Minimum Match 0%
Maximum Match 100%
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Maximum DB
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A_Geneseq_19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
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2378
1 MDHQDPYSVQATAAIAAAIT.....QDFRRAFRRILCRPWTQTAW 450
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1873.391 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARII

9	80	7	6	ភ	4	w	2	_	Regult No.	
2329	2329	2351.5	2351.5	2351.5	2370	2378	2378	2378	Score	
97.9	97.9	98.9	98.9	98.9	99.7	100.0	100.0	100.0	Query Match Length DB	dP
487	487	447	447	447	450	450	450	450	Length	
18	12	23	22	22	24	23	22	22	B .	
AAW11804	AAR14149	AAE26633	AAE00989	AAM52118	ABP81780	AAE26634	AAE00990	AAM52117	ID	
Human alpha-2b adr	Human alpha 2 beta	Human alpha-2B-adr	Human alpha2B-adre	Human alpha-2BAR t	Human alpha 2b-adr	Human alpha-2B-adr	Human alpha2B-adre	Human alpha-2BAR t	Description	

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24.6	24.6	24.7	24.7	24.7	24.7	24.7	•		•				•		27.4	27.4	•				41.4	41.7	42.1	42.1			•	•	•	•	•	7.	7.		68.3
517	515	520	515	515	415	467	467	415	415	415	467	476	379	601	601	601	601	307	307	330	330	324	330	330	334	334	458	461	461	457	450	450	450	330	330
21	22	15	16	15	17	17	15	20	11	24	24	18	18	23				22		17	15	10	17	15	17	15	15	24	22	22	24	22	22	17	15
AAY57169	AAU05408	AAR52831	AAR90041	AAR70995	AAW09388	AAR96215	S	AAY01598	AAR05539	ABG73546	ABP81811	AAW24089	AAW33185	AAE17036	AAG80701	ABB63318	AAR21931	AAU08334	ABG73538	AAW02670	AAR48698	AAP90552	AAW02672	AAR48700	AAW02673	AAR48701	AAR54834	ABP81781	AAM52124	212	ABP81779	AAM52122	AAM52123	AAW02671	AAR48699
Sequence of HuAlph	reno	a		Human/rat alpha-1B	Mouse dopamine D2	Recombinant human	Sequence encoded b	D2	Rat D2 dopamine re	Rat dopamine D2 re	Human dopamine rec	Balanus amphitrite	Corn barnacle G-pr	Drosophila melanog	D. melanogaster oc	Drosophila melanog	D.melanogaster oct	Human alpha 2 adre	ha2-a	G-protein coupled	Ħ	Hamster beta-2 -ad			G-protein coupled		derive	alpha 2c-ad		alpha-	u	Human alpha-2AAR p	Human alpha-2AAR v	G-protein coupled	G-protein coupled

# ALIGNMENTS

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RESULT 1
AAMS2117
ID AAMS
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AC AAMS
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AC Huma
XX Huma
XX Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-FEB-2002 (first entry)
    WO200179561-A2
                                                                                                                         Domain
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                                                                                                                                                                                                                                                                                                                                                              Region
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                                                                                                                         /label=
373..396
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/note= "featured in figure 2"
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25-OCT-2001

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                                                                                                                                                                                                                                                                                                                                                                            (C) (b) detecting a polymorphic site comprising nucleotide positions 901-909 (C) or a site comprising cyrosine or guanine at position 753 of (IIV) (C) or a site comprising (A) (93996999669) or (B) (939999693) at (C) positions 961-972 of (III). The method may be used for genotyping an (C) alpha2B, alpha2A or alpha2C receptor gene and further used to determine (C) associated with alpha2B, alpha2A or alpha2A or alpha2, comprising detecting a (C) disease, central nervous system disease end combinations of these. In (C) combinations of these or alpha2A, or alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, clonidine, oxymetazoline, guanaberz, UK14304, BH7933 and (C) combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, C) these) by detecting the polymorphic site and correlating the site to a (C) cyclase, MAP kinase activity, phosphorylation or inositol phosphate (the human alpha-2BAR protein, the sequence is that of the third intracellular loop of complying site at residues 301-303 (EEE), absent in the alpha-2BAR
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                 Matches 450;
                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (I)-(III) by detecting a polymorphic site, comprising; (a) obtaining a sample having a polymucleotide encoding an alpha-2B, alpha2A or alpha2C or fragment or complement of; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; Page 146-147; 163pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting a polymorphic site .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-APR-2000; 2000US-0551744.
10-AUG-2000; 2000US-0636259.
19-OCT-2000; 2000US-0692077.
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                                                     181
                                                                                 181
                                                                                                             121 NSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGS
                                                                                                                                                                            19
                                                                                                                                                                                                         61
                                                                                                                                                                                                                                     1 MDHQDPYSVQATAAIAAAITELILETIFGNALVILAVLTSRSLRAPQNLFLVSLAAADIL
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DB; AAI99905.
ASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEEE
                             PPAPCLIMILVYLRIYLIAKKSNRRGPRAKGGPGQGESKQPRÞÞHGGALASAKLPALASV
                                                 FFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALASV
                                                                                         NSKRTPŘŘÍKĆTÍLTVÁLIAAVISLPPLIYKGDÓGPOPŘGŘPÓCKLNOBAMYTLASSIGS
                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                         VATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEY 120
                                                                                                                                                                                                                 mdhodpysvoátaatáaattélilettegnalvílávítskéleaþonlelvslaaadtl
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Pred. No. 2
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RESULT 2
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The present sequence is human alpha2B-adrenoceptor (alpha2B-AR) protein. Alpha2B-AR has a glutamic acid repeat element (amino acids 298-399) of 294-311), located in the third intracellular loop of the receptor mediate many of the physiological effects of the catecholamines, norepinephrine and epinephrine. An antagonist of alpha2B-AR norepinephrine and epinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating a mammal suffering from vascular contraction of coronary arteries which is clinically expressed as coronary heat disease (CHD), unstable chronic angina pectoris which is clinically expressed as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
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                                                                                                                                                     Disclosure; Page 29-31; 37pp; English.
                                                                                                                                                                                 New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of coronar
                                                                                                                                                                                                                                                                                                      Snapir A,
                                                                                                                                                                                                                                                                                             Scheinin
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                                                                                                                                                                                                                                                                                                                         (JUVA-) JUVANTIA PHARMA
                                                                                                                                                                                                                                                                                                                                                                                                                         WO200129082-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      norepinephrine; epinephrine; therapy; vascular contraction; coronary artery; coronary heat disease; CHD; chronic angina pectoris; acute myocardial infarction; AMI; Prinzmetal's variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR; glutamic acid repeat; intracellular loop; chromosome 2; catechol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human alpha2B-adrenoceptor (alpha2B-AR) protein.
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DB; AAD04762.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQLTREKRETEVLÁVVÍGVEVLCWEPFFFSYSLGAÍCFKHCKVPHGLFQFFFWIGYCNSS
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298..309
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JT, Tuomainen T,
J, Valkonen V;
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ARESULT 3
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Detecting a risk of hypertension and targeting treatment
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04-MAR-2003
Human alpha

2b-adrenoceptor protein SEQ ID NO:42.

standard;

Protein;

G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; growth-related disease; generation-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;

hypertension; hypotension; ulcer.

renal

disorder; rheumatoid

trauma;

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the antihypertensive effect of compounds. The present sequence is alpha-2B-adrenoceptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method for detecting a risk of hypertension by determining the pattern of alleles encoding a variant alpha-2B-adrenoceptor (AR) protein. The methods and compositions of the invention are useful for detecting risks and targeting treatment for hypertension. The kit is also useful for selecting for clinical drug trials testing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by determining the pattern of alleles encoding
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                   LNPVIYTIFNQDFRRAFRRILCRPWTQTAW 450
                                                                                                                                                                                                                                                                                                           NSKRTPRRIKCIILTWWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGS
                                                                                                                                                                                                                                                                                                                               NSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGS
                                                                                                                                                                                                                                                                                                                                                                                          VATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEY
LNPVIYTIFNQDFRRAFRRILCRPWTQTAW 450
                                                            AQLTREKRETEVLAVVIGVEVLCWEPFFFSYSLGAICPKHCKVPHGLFQFFFWIGYCNSS
                                                                              AQLTREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPKHCKVPHGLFQFFFWIGYCNSS
                                                                                                                        EEEEEEEEECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRR
                                                                                                                                           EEEEEEEEECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGGWWRRR
                                                                                                                                                                                      ASAREVNGHSKSTGEKEEGET PEDTGTRAL PPSWAAL PNSGQGQKEGVCGAS PEDEAEEE
                                                                                                                                                                                                        ASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEEE
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                                                                                                                                                                                                                                                                     FFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALASV
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08-AUG-2002

WO200261087-A2 Homo sapiens

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                                                                                                                                                                                                                                                                                                                                                         The present invention describes antigenic peptides (I) comprising:
CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular
CC and (2) an isolated antibody having high specificity and high affinity
CC and (2) an isolated antibody having high specificity and high affinity
CC antibody against a particular GPCR. (I) can be used as GPCR modulators and
CC an antibody against a particular GPCR, and in the production of specific
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC creating immune-related diseases, growth-related diseases, cell
CC diseases, or autoimmune diseases, e.g. AlDS, Alzheimer's disease,
CC diseases, or autoimmune diseases, e.g. AlDS, Alzheimer's disease,
CC atheroscierosis, bacterial, fungal, protozoan or viral infections,
CC diseases, Parkinson's disease, and tiple sclerosis, pain, psoriasis,
CC disease, Parkinson's disease, diabetes, graft versus host
CC disease, Parkinson's disease, diabetes, graft versus host
CC disease, Parkinson's disease, diabetes, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC any other disorder in which GPCRs are involved. The antibodies may be
CC GPCR proteins given in ABB81675 to ABB82018, which are used in the
CC exemplification of the present invention.
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Best Local S
Matches 448
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FFAPCLIMILVYLRIYLIAKRŚNRRGPRAKGGPGGESKOPRÞDHGGALÁSAKLPALASV
                     FFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALASV
                                                                                         NSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQBAWYILASSIGS
                                                                 NSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQBAWYILASSIGS
                                                                                                                                                           VATLIIPESLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEY
                                                                                                                                                                                                                             MDHQDPYSVQATAAIAAAITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADIL
                                                                                                                                     VATLÍ Í PFSLÁNELLGYMYFRRTWCEVYLALDVLFCTSS Í VHLCÁ Í SLDRYMAVSRÁLEY
                                                                                                                                                                                                       MDHODPYSVQATAAIAAAITFLILFTIFGNALVILAVLTSRSLRAPONLFLVSLAAADIL
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Pred. No. 1e-193;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                   invention.
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                                                                                                                                                                                                                                                                                                             Length 450;
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The invention relates to genotyping an alpha-2B, 2A, or 2C adrene receptor gene (I)-(III) by detecting a polymorphic site, comprisi (a) obtaining a sample having a polymoleotide encoding an alpha-2h or alpha-2C or fragment or complement of; and (b) detecting a polymorphic site comprising nucleotide positions of (I), a site comprising cytosine or guanine at position 753 of

or 2C adrenergic ite, comprising; ing an alpha-2B,

Claim 20;

Page 147-149;

163pp;

English

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RESULT 5
AAM52118
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                                                                                  Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting a polymorphic site -
                                                                                                                                                                                 (LIGG/)
                                                                                                                                                                                                           17-APR-2000; 2000US-0551744
10-AUG-2000; 2000US-0636259
19-OCT-2000; 2000US-0692077
                                                                                                                                                                                                                                                17-APR-2001; 2001WO-US12575
                                                                                                                                                                                                                                                                                                                                                                                                             Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity
                                                                                                                                                                                                                                                                                          WO200179561-A2
                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                     Key
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                                                                                                                                                                                                                                                                                                                                                             Domain
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SMALL K M.
                                                                                                                                  AAI99906
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370..393
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                                                                                                                                                                                                                                                                                                        label= transmembrane_domain
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                                                                                                                                                                                                                                                                                                                                              abel= transmembrane_domain
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Best Local S
Matches 447
Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR; glutamic acid repeat; intracellular loop; chromosome 2; catecholamine; norepinephrine; epinephrine; therapy; vascular contraction; variant; coronary artery; coronary heat disease; CHD; chronic angina pectoris;
                                                                                                                                                                                                                   04-JUL-2001
                                                                                                                                                     Human alpha2B-adrenoceptor (alpha2B-AR) variant
                                                                                                                                                                                                                                                                              AAE00989
                                                                                                                                                                                                                                                                                                                                      AAE00989 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEEEEEEECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRR
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Pred. No. 3.9e-192;
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Scheinin M
                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of corona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; Page
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ASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEEE 300
                                                                                          NSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGS
                                                                                                                                                  VATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEY
                                                    FFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALASV
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                                                                                                                                                                                                                                                                                                                     447 AA;
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                                                                                                                                                                                                                                                                           98.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is human alpha2B-adrenoceptor (alpha2B-AR) variant
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, Tuomainen T,
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                                                                                                                                                                                                                                                           Score 2351.5; DB 2;
Pred. No. 3.9e-192;
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T, Lakka
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Nyyssoenen
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                                                                                                                                                                           Sequence
                                                                                                                                                                                                 The invention relates to a method for detecting a risk of hypertension by determining the pattern of alleles encoding a variant alpha-2B-adrenoceptor (AR) protein. The methods and compositions of the invention are useful for detecting risks and targeting treatment for hypertension. The kit is also useful for selecting for clinical drug trials testing the antihypertensive effect of compounds. The present sequence is human
                                                                                                                                                                                              alpha-2B-adrenoceptor variant.
                                                                                                                                                                                                                                                                                                                      Detecting a risk of hypertension and targeting treatment by determining the pattern of alleles encoding a variant
                                                                                                                                                                                                                                                                                       Disclosure; Page 26-27; 35pp; English.
                                                                                                                                                                                                                                                                                                                   alpha-2-adrenoceptor
                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAD44388.
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                                                                                                                                                                                                                                                                                                                                                                                                      Salonen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human alpha-2B-adrenoceptor variant.
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447; Conserva
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NSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGS
                       VATLIIPPSLANELIGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEY 120
                                                                     MDHODEYSVOATAATAAATTELILETTEGNALVILAVLTSRSLRAEONLELVSLAAADIL
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                                                                                                                           Conservative
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                                                                                                                   Score 2351.5; DB 23; Length 447; 
Pred. No. 3.9e-192; 
0; Mismatches 0; Indels 3;
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                                                                                                                                                              Clone NGC-alpha2beta was isolated from a human spleen genomic library by screening with a fragment of the human 5-HTLA receptor gene. The gene was used to express recombinant receptor protein which can be used to produce antibodies for inhibition of receptor
                                                                                                            Sequence
                                                                                                                                                                                                                                                                                       Disclosure; Fig 2; 15pp; English
                                                                                                                                                                                                                                                                                                                                                Isolated DNA encoding human adrenergic receptor - for detecting nucleic acids encoding alpha, 2-beta adrenergic receptor, for
                                                                                                                                                            function.
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  Score 2329; DB 12;
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  Human alpha-2B adrenergic receptor (AAW11804) is a member of the rhodopsin-like signal transducer family. Its amino acid sequence was deduced from a genomic DNA clone (AAT59499) obtd. from a hume spleen DNA library. Vectors have been adapted to allow prodn. of
                                                                                                                                                                                                                                    WPI; 1997-107576/10.
N-PSDB; AAT59499.
                                                                                                                                                                                                                                                                                                                                                                                                                         30-OCT-1989;
30-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alpha-2b adrenergic receptor; adrenoceptor; adrenaline; epinephrine; signal transduction; neurotransmitter; ligand.
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06-MAY-1997
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 G-protein coupled receptor; ligand binding assay; transmembrane domain;
                                 G-protein coupled human alpha-2 C2 adrenergic receptor.
                                                                  25-MAR-2003
12-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTFRRIKC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAAIAAAITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADILVATLIIPFSLA 71
                                                                                                                                                                                                                                                         DFRRAFRRILCRPWTQTAW 450
                                                                                                                                                                                                                                                                                                  VLAVVIGVEVICWEPEFFSYSLGAICPKHCKVPHGLFQFFFWIGYCNSSLNPVIYTIFNQ 312
                                                                                                                                                                                                                                                                                                                               VLAVVIGVEVLCWEPFFFSYSLGAICPKHCKVPHGLFQFFFWIGYCNSSLNPVIYTIENQ
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(first en
                                                                  entry)
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73.1%;
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(Updated on 25-WAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-SEP-1993;
10-SEP-1992;
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                                                                                                                                                                                                                                                                                                                                                                                YLRIYLIAKRSNRRGGPRAKGGPGQGESKQPRPDHGGALASAKLPALASVASAREVNGHSK 251
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                              VLAVVIGVEVLCWFEFFFSYSLGAICDKHCKVDHGLFQFFFWIGYCNSSLNEVIYTIFNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGSFFAPCLIMILV 191
                                                                                                                                                PQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFTF 371
                                                                                                                                                                                                                                                                                        STGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEEEEEEEEEEECE
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92US-0943236.
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Pred. No. 2.8e-130;
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CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic CC receptor gene (I)-(III) by detecting a polymorphic site, comprising; CC (a) obtaining a sample having a polymucleotide encoding an alpha-2B, CC alpha2A or alpha2C or fragment or complement of; and CC (b) detecting a polymorphic site comprising nucleotide positions 901-909 CC of (I), a site comprising cytosine or guanine at position 753 of (IIV) CC or a site comprising (A) (ggggggggccg) or (B) (gggggggtggg) at CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine CC whether an individual is at increased risk of developing a disease CC associated with alpha2B, alpha2A or alpha2, comprising detecting a CC polymorphic site which correlate to disease selected from cardiovascular CC disease, central nervous system disease and combinations of these. In CC addition, the technique may be used to predict an individual's response CC norepinephrine, clonidine, oxymetascilne, guanabanz, UK14304, BHT933 and CC combinations of these) or antagonist (e.g. pinephrine, prazosin, ARC 239, CT anwolscine, idazoxan, tolazoline, phentolamine and combinations of these or antagonist (e.g. yohimbine, prazosin, ARC 239, CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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10-AUG-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 48; Page 154-155; 163pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-APR-2001;
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Best Local :
                                                    17-APR-2000; 2000US-0551744
10-AUG-2000; 2000US-0636259
19-OCT-2000; 2000US-0692077
                                                                                                                                                                                Human; genotyping; alpha-2B; alpha-2A; alpha-2G; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity phosphorylation; inositol phosphate; alpha-2AAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
  Liggett
                       (LIGG/)
(SMAL/)
                                                                                                                                                                                                                                    Human alpha-2AAR protein.
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                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                            LFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCR
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                                                                                                                                                                                                                                                                                                                                                                                                           --VGAIGGQWWRRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPKHCKVPHG 406
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Pred. No. 1.2
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CC of (I), a site comprising cytosine or guanine at position 73 of (IIV)

CC of (I), a site comprising cytosine or guanine at position 73 of (IIV)

CC or a site comprising (A) (gyggggggcg) or (B) (gygggggtgag) at CC positions 961-972 of (III). The method may be used for genotyping an CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine CC whether an individual is at increased risk of developing a disease CC associated with alpha2B, alpha2A or alpha2, comprising detecting a CC polymorphic site which correlate to disease selected from cardiovascular CC disease, central nervous system disease and combinations of these. In CC disease, central nervous system disease and combinations of these. In CC combinations, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and CC combinations of these) or antagonist (e.g. epinephrine, contral the contral capture, guanabenz, UK14304, BHT933 and CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, CC rauwolscine, idazoxan, tolazoline, phentolamine and combinations of these) by detecting the polymorphic site and correlating the site to a correlating the contral response (where the response is correlated to adenylyl CC cyclase, MAP kinase activity, phosphorplation or inositol phosphate CC levels). The present sequence is that of the human alpha-2AAR protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                      SDHAERPPGPRRPERGPRGKGKARASQVKPGD--SLPRRGPG-----ATGIGTPAAGPGE
                                                                      --VGAIGGQWWRRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYSIGAICFKHCKVPHG
 LEKPEFWEGYCNSSLNEVIYTIENHDERRAFKKILCR
              LFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCR 443
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                                               The present invention describes antigenic peptides (1) comprising:

CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino CC (a) any one of a particular CC (a) any of a particular (GPCR) or a candidate polypeptide in a sample; CC and (2) an isolated antibody having high specificity and high affinity CC (a) any otherways. The antigenic peptides for GPCRs are useful in detecting CC an intibodies. The peptides and antibodies are useful for detecting the CC antibodies. The peptides and antibodies are useful for detecting the CC presence or absence of corresponding GPCRs. The antigenic peptides for CC gPCRs and antibodies are useful for diagnosing and designing drugs for CC treating immune-related diseases, from the related disease, cell proliferative CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, CC atherosclerosis, bacterial, fungal, protozoan or viral infections, CC anxiety, depression, schizophrenia, dementia, mental retardation, memory CC anxiety, depression, schizophrenia, dementia, mental retardation, memory CC anxiety, depression, schizophrenia, dementia, mental retardation, wemory consisting of the present involved. The antibodies may be CC consisted in immunoassays and immunodiagnosis. ABZ42523 to ABZ42669 encode cxemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; GPCR; antibody; immune-related disease; and is growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzeiner's disease; atteroscierosis; infection; osteoparthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma; hypertension; hypotension; renal disorder; rheumatoid arthritis;
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Best Local Similarity
                                 17-APR-2000;
10-AUG-2000;
19-OCT-2000;
                                                                                                                                                                                                                                               Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity phosphorylation; inositol phosphate; alpha-2CAR.
(LIGG/)
                                                                               17-APR-2001; 2001WO-US12575.
                                                                                                                                                                Domain
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SMALL K M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAIGGQWWRRRAQL---TREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPKHCKVPHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDEAEE----EBEEEBEBEBCBPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGV 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SASGLP--RRRAGAGGONLEKRFTFVLAVVIGVFVVCWFPFFFTYTLTAV---GCSVPRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDHAERPPGPRRPERGPRGKGKARASQVKPGDSLRGAGRGRRGS-----GRRLQGRGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRRIKATITTCWVISAVISFPPLISIEKKGGGGGPQP-AEPRCEINDQKWYVISSCIGSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYSLQVTLTLVCLAGLLMLLTVFGNVLVIIAVFTSRALKAPQNLFLVSLASADILVATLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.0%; Score 1117.5; DB 24; Length 450; ilarity 52.7%; Pred. No. 7.1e-87; Conservative 52; Mismatches 105; Indels 59;
                                  2000US-0551744.
2000US-0636259.
2000US-0692077.
                                                                                                                                                                                     Location/Qualifiers
208..231
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Matches 240;

Local

Similarity

Conservative

40;

Indels

79;

Gaps

12

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351

404

PHGLFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCR

FLSRRRRARSSVCRRKVAQ-AREKRFTFVLAVVMGVFVLCWFPFFFIYSLYGICREACQV

409

LLGRGVGAIGGQWWRRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFFSYSLGAICPKHCKV

183 166 127 106 67 46 7

RRIKCIILTVWLIAAVISLPPLI--YKGDQGPQPRGR--PQCKLNQEAWYILASSIGSFF

PFSLANELLGYWYERRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTP 126

PFSLANELMAYWYFGQVWCGVYLALDVLFCTSSIVHLCAISLDRYWSVTQAVEYNLKRTP

YSVQATAAIAAAITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADIILVATLII 66

YSAGAVAGLAAVVGFLIVFTVVGNVLVVIAVLTSRALRAPQNLFLVSLASADILVATLVM

105

RRVKATIVAVWLISAVISFPPLVSLYR-----QPDGAAYPQCGLNDETWYILSSCIGSFF

APCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALASVAS

221

APCLIMGLVYARIYRVAKRRTR-------

-----TLSEKRAPVGPDGAS

257 242 220

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310

258

PTTENGLGAAAGEAR--

AREVNGHSKSTGEKEEGETPEDTGT-RALPPSW-----AALPNSG-----

TGTARPRPPTWSRTRAAQRPRGGAPGPLRRGGRRRAGA

KEGVCGASPEDEAEEEEEEEEEEEEEECEPQAVPVSPASACSPPLQQPQGSRVLATLRG-QV

------GALTASRSP--GPGGRLSRASSRSVEF

EGGAGGADGQGAAES---

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CC (b) detecting a polymorphic site comprising nuclectide positions 901-909 CC of (I), a site comprising cytosine or guanine at position 753 of (IIV) CC or a site comprising (A) (ggggcggggcg) or (B) (ggggcggtggg) at CC positions 961-972 of (III). The method may be used for genotyping an CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine CC whether an individual is at increased risk of developing a disease CC associated with alpha2B, alpha2A or alpha2, comprising detecting a CC polymorphic site which correlate to disease selected from cardiovascular CC disease, central nervous system disease and combinations of these. In CC addition, the technique may be used to predict an individual s response to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, CC rauwolscine, idazoxan, tolazoline, phentolamine and combinations of these) by detecting the polymorphic site and correlating the site to a CC predetermined response (where the response is correlating the site to a CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate CC levels). The present sequence is that of the human alpha-2CAR variant CC protein, deleted for a 4 amino acid polymorphic site at residues 321-324 of the wildtype protein (AAM52124).
                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting a polymorphic site -
                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha2A or alpha2C or fragment or complement of; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to receptor gene (I)-(III) k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 78; Page 160-162; 163pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to genotyping an alpha-2B, 2A, or 2C adrenergi eptor gene (I)-(III) by detecting a polymorphic site, comprising, obtaining a sample having a polynucleotide encoding an alpha-2B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SB,
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                                                                                                  457 AA;
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                       45.4%;
Score 1079.5; DB 22
Pred. No. 1.3e-83;
0; Mismatches 101;
                                                 22;
                                                 Length
                                                 457;
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Search completed: February 6, 2004, 18:17:31 Job time : 40.1271 secs 

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Result
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Maximum Match 100%
Listing first 45 summaries
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /cgn2 6/ptodata/1.
3: /cgn2 6/ptodata/1.
4: /cgn2 6/ptodata/1.
5: /cgn2 6/ptodata/1.
6: /cgn2_6/ptodata/1.
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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PCT-US93-08528-20
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          Sequence 20, Appl
Sequence 20, Appli
Sequence 5, Appli
Sequence 4, Appli
Sequence 22, Appli
Sequence 22, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 19, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 22, Appli
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3 US-09-206-899-22 1 US-08-334-698-4 1 US-08-228-932-4 1 US-08-468-939-4 1 US-08-468-939-4 2 US-08-722-190-4 2 US-08-722-190-4 3 US-09-206-899-4 3 US-09-206-899-4 4 US-09-688-415-10 1 US-08-248-15-10 1 US-08-268-415-10 1 US-08-68-415-10 1 US-08-68-415-10 1 US-08-68-415-10 1 US-08-68-415-10 1 US-08-68-415-10 1 US-08-68-611-20 2 US-09-68-694-20 3 US-09-606-694-20 4 US-09-378-074-20	419	419	419	419	419	515	520	520	520	520	520	520	520	520	520	520	515	
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000000000000000000000000000000000000000	App	Appl	Appl	App1	Appli	App1	Appli	Appl	App1	App1	App1	App1	App1:	Appli	Appli	Appli	Appl	- 72.

ALIGNMENTS

#### US-08-118-270-20 RESULT 1 US-08-118-270-20 Sequence 20, Apprint No. 5508384 COMPUTER: IBM PC COMPATIBLE COMPATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Ve. SOFTWARE: PATENTIN Release #1.0, Ve. CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/118,270 FILING DATE: 09-SEP-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/943,236 APPLICATION NUMBER: US 07/943,236 FILING DATE: 10-SEP-1992 ATTORNEY/AGENT INFORMATION: NAME: Townsend, Kevin G. REGRISTRATION NUMBER: 34,033 REFERENCES/DOCKET NUMBER: MURPHY=2A TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEFAX: 202-737-3528 TELEX: 248633 INFORMATION FOR SEQ ID NO: GENERAL INFORMATION: APPLICANT: Murphy, Randall B. APPLICANT: Schuster, David I. TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF NUMBER OF SEQUENCES: 348 CORRESPONDENCE ADDRESS: ADDRESSEE: BROWDY AND NEIMARK STREET: 419 Seventh Street, N.W., Suite 300 SEQUENCE CHARACTERISTICS: LENGTH: 330 amino acids COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk MOLECULE TYPE: peptide TYPE: amino acid STRANDEDNESS: sir TOPOLOGY: linear COUNTRY: U ZIP: 20004 STATE: D.C CITY: Washington Application US/08118270 202-737-3528 USA SS: single linear 20: MURPHY=2A Version #1.25

Matches 321; Query Match Best Local Similarity

Conservative

6;

Score 1624.5; DB 1; Pred. No. 5.9e-100; 6; Mismatches 3;

DB 1;

Indels 109; Length 330;

Gaps

4

68.3%; 73.1%;

Indels 109; Length

Gaps

226

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RESULT 2
PCT-US93-08528-20
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GENERAL INFORMATION:
APPLICANT: New York University
                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                      NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                               FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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STREET: Washington
CITY: Washington
CTATE: D.C.
TTATE: TTATE
  TOPOLOGY: 1
MOLECULE TYPE:
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                                                                                                                           TELEFAX: 248633
            TYPE:
STRANDEDNESS: SIL
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419 Seventh Street, N.W.,
peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                  APPLICATION NUMBER: US/08/
FILING DATE: 08-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: ISTACISCH, NEC A.
REGISTRATION NUMBER: 29,65
REFERENCE/DOCKET NUMBER: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Venter, John C.
APPLICANT: Fraser, Claire M.
APPLICANT: MCCombie, William R.
TITLE OF INVENTION: OCTOPAMINE RECEPTOR
                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 620 Newport
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                 ZIP: 92660
                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                         STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEEEEEEEEEEEEE 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFTF 371
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                                                                                                                                                                                                                                                                                                                                                                    USA
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73.1%;
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Pred. No. 5.9e-100;
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                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08444734A Patent No. 5610282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Sibley,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: pr
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: in
                                                                                                                                                             APPLICANT: Monsma, Frederick J.
APPLICANT: Mahan, Lawrence C.
APPLICANT: McVittie, Loris D.
TITLE OF INVENTION: cDNA encoding the rat D1 dopamine
TITLE OF INVENTION: exceptor linked to admylyl cyclase
TITLE OF INVENTION: expression of the receptor protein
TITLE OF INVENTION: cell lines
                                                                                                                         NUMBER OF SEQUENCES: 1
ZIP: 92660
COMPUTER READABLE FORM:
                                                   STREET: 620 No. Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 PRRIKCIILTVWLIAAVISLPPLI----YKGDQGPQPRGRPQCKLNQEAWYILASSIGSF 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SASGLP--RRRAGAQGQNREKRFTFVLAVVIGVFVVCWFPFFFTYTLTAV---GCSVPRT 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAIGGQWWRRRAQL---TREKRETFVLAVVIGVEVLCWEPFFEFSYSLGAICPKHCKVEHG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDHAERPPGPRRPERGPRGKGKARASQVKPGDSLRGAGRGRRGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEPLPT----QLNG---APGEPAPA-GPRDTDALDLEES------SS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAPCLIMILVYVRIYQIAKRTRVPPSRRGPDAVAAPPGGTERRPNGLGPERSAGPGGAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAPCLIMILVYLRIYLIAKR-----SNRRGPRAKGGPGQGESKQPR---PDHGGALASAK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRRIKAILITVMVISAVISFPPLISIEKKGGGGGPQP-AEPRCEINDQKMYVIASCIGSF 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | IPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYSVQATAAIAAAITFLILETIFGNALVILAVLTSRSLRAPQNLFLVSLAAADILVATLI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDEAEE----EEEEEEEEECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGV 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I PFSLANEVMGYWYFGKTWCEIYLALDVLFCTSSIVHLCAISLDRYWSITQAIEYNLKRT
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                                                                                       3E: Knobbe, Martens, Olson and Bear
620 Newport Center Drive, Sixteenth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      450 amino acids
                                    USA
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PRIOR APPLICATION NUMBER: US 07/548
APPLICATION NUMBER: US 07/548
FILING DATE: 06-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: NIHO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (714) 760-9502
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
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APPLICATION NUMBER: US 01
FILING DATE: 03_MAR-1993
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OPERATING SYSTEM: PC-DOS/MS-DOS
SODTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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CLASSIFICATION:
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COMPUTER: IE
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                                                                                                                                                                                                                                                                                                                                PRRIKCIILTVWLIAAVISLPPLI----YKGDQGPQPRGRPQCKLNQEAWYILASSIGSF 181
                 LFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCR 443
                                                                 SÄSGLP--RRRÄGAGGONREKRFTFVLÄVVIGVFVVCWFPFFFTYTLTÄV---GCSVPRT 406
                                                                                 GAIGGQWWRRRAQL---TREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICFXHCKVPHG 406
                                                                                                                                                                                                 AEPLPT----QLNG---APGEPAPA-GPRDTDALDLEES--
                                                                                                                                                                                                                                                                                       FAPCLIMILVYLRIYLIAKR-----SNRRGPRAKGGPGQGESKQPR---PDHGGALASAK 233
                                                                                                                                                                                                                                                                                                                                                                                                  IPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRT 125
LFKFFFWFGYCNSSLNPVIYTIFNHDFRRAFKKILCR
                                                                                                                               SDHAERPPGPRRPERGPRGKGKARASQVKPGDSLRGAGRGRRGS-----
                                                                                                                                                            EDEAEE ---- EEEEEEEEEECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGV 349
                                                                                                                                                                                                                                                                 FAPCLIMILVYVRIYQLAKRRTRVPPSRRGPDAVAAPPGGTERRPNGLGPERSAGPGGAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYSLQVTLTLVCLAGLLMLLTVFGNVLYIIAVFTSRALKAPQNLFLVSLASADILVATLV
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52.7%;
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443
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RESULT 5 US-08-194-338-4

Sequence 4,

Application US/08194338

Patent No. 5474898 GENERAL INFORMATI

INFORMATION:

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Best Local
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SEQUENCE CHARACTERISTICS:
LENGTH: 461 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NC
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NII
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEPAX: (619) 235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Venter, John C.
APPLICANT: Venter, John C.
APPLICANT: Framer, Claire M.
APPLICANT: MCCOmbie, William R.
TITLE OF INVENTION: OCTOPAMINE RECEPTOR
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
STREET: 620 Newport Center Drive, Sixteenth Floor
STRIE: CA.
COLUMNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Israelsen, Ned A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 08-FEB
                          285 KEGVCGASPEDEAEEEEEEEEEEEEEEEPQAVPVSPASACSPPLQQPQGSRVLATLRG-QV 343
                                                                                                       243
                                                                                                                                            183 APCLIMILVYLRIYLIAKRSNRRGFRAKGGFGQGESKQFRPDHGGALASAKLPALASVAS 242
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                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                                                           n 44.7%; Score 1063.5; DB 1; Length 461; Similarity 51.3%; Pred. No. 7.2e-63; 36; Conservative 43; Mismatches 106; Indels 75.
                                                                      PTTENGLGAAAGEAR.
                                                                         APCLIMGLVYARIYRVAKRTR-----
                                                                                                                                                                                                 RRIKCIILTVWLIAAVISLPPLI--YKGDQGPQPRGR--PQCKLNQEAWYILASSIGSFF 182
                                                                                                                                                                                                                                                     PFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTP 126
                                                                                                                                                                         RRVKATÍVAVWIÍSAVIŠFÞÞLVSLYR-----ÓÞDGAAYÞÓCGLNDÉTWÝÍLSSCIQSFF
                                                                                                                                                                                                                                  PFŚLANELMAYWY FGQVWCGVY LALDVL FCTSS I VHLCATSLDRYWSVTGAVEYNLKRTP
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-DGQGAGPGAAQSGALTASRSP--GPGGRLSRASSRSVEF
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                                                        -TGTARPRÞÍTWÁRTRAAQRÞRGGAÞGÞLRRGGRRRAGA 310
                                                                                                                                                                                                                                                                                                                                                       ed. No. 7.2e-63;
Mismatches 106; Indels
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US-08-118-270-22
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TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: lin
MOLECULE TYPE:
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REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MU
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA,
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA;
TOTALING SYSTEM TO TOTALING TO TOTALING TO TOTALING TO TOTALING TO TOTALING TO TOTALING TO TOTALING TO TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALING TOTALI
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ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.,
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APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPERFIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 334 amino acids
TYPE: amino acid
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                                                 188 MILVYLRIYLIAKR-----SNRRGPRAKGGPGQGESKQPR----PDHGGALASAKLPALAS 239
                              180
                                                                                                                                             132 IILTYWLIAAVISLPPLIY----KGDQGPQPRGRPQCKLNQBAWYILASSIGSFFAPCLI 187
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NHĽVÝVŘÍ ÝQÍÁKRTRVEPSKRGEDÁCSA PEGGADRRENA VGÉERGAGTA ---
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5. 5508384
                                                                                                     IIVTVWVÍSAVÍSFÞÞÍLISIEKKGAGGGQQPAEÞSCKINDQKWYVISSSÍGSFFÁÞCLÍ 179
                                                                                                                                                                                                                                                             NELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTPRRIKC 131
                                                                                                                                                                                                                        NEVM-YWYFGKVWCEIYLAIDVLFCTSSIVHLCAISLDRYWSITQAIEYNLKRTPRRIKA 119
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Pred. No. 1.2e-60;
6; Mismatches 59;
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PCT-US93-08528-22
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                                                                                                                                         Matches
                                                                                                                                                      Query Match
Best Local Similarity 47.3%;
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APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                       TENGTH: 334 amino
TYPE: amino acid
STRANDEDNESS: sing
STRANDEDNESS: sing
TOPOLOGY: linear
MOLECULE TYPE: pepti
                                                                                                                                                                                                                                                                                                                                                                                 NAME: Townsend, Kevin G.
REGIZION NUMBER: 34,033
REFERENCEIDOCKET NUMBER: MUI
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-628-5197
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TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy
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ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.,
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                           NELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTPRRIKC 131
                                                                SLNPVIYTIFNHDFRRAFKKILCR 327
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NEVM-YWYFGKVWCEIYLAIDVLFCTSSIVHLCAISLDRYWSITQAIEYNLKRTPRRIKA 119
                                                                                                                                                                                                                                                                                               334 amino acids
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                                                                                                                                         Conservative
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                                                                                                                                                                                                                                            ss: single
linear
                                                                                                                                                                                                                           peptide
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                                                                                                                                     ; Score 1027.5; DB 5; Length 334; ; Pred. No. 1.2e-60; 46; Mismatches 59; Indels 129;
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Patent No. 594241
                                                                               Query Match
Best Local (
                                                                 Matches
                                                                                                                                                                                                                                TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 3256
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Yi Li and Mark D. Adams
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Human G-Protein Receptor HIBEF51 NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA: US
                                                            43.1%; Score 1025.5; DB 2; Local Similarity 48.4%; Pred. No. 1.8e-60; hes 218; Conservative 39. Microscore
                                                                                                                                                              LENGTH: 358 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 06-JUN
CLASSIFICATION: 536
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STATE: NJ
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SLNPVIYTIFNQDFRRAFRRILCR 443
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EE: Cecchi, Stewart & Olstein
6 Becker Farm Road
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                                                                 Indels
                                                                                              Length 358;
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                                                               137;
                                                                 Gaps
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Gaps

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APPLICATION UNMER: US/08/118,270
PRIOR APPLICATION UNMER: US/07/943,236
APPLICATION UNMER: US 07/943,236
APPLICATION UNMER: US 07/943,236
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSEND, SEVEND, SEREFERICE/DOCKET NUMBER: MIRPHY=2A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHNUE: 202-28-5197
                                                                                                  TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21, Application US/08118270 Patent No. 5508384
                                                                                                                                                                                                                                                                                                                                                 ZIP: 20004

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
                                                   LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MUIDHY, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
                                                                                                                                              TELEPHONE: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 419 Seven CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206 CÍGSFFAÞCLÍMÍLVÝVRÍYQÍAKRTRVÞÞSRRG-----
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   MEDIUM TYPE: FLORY:

MEDIUM TYPE: FLORY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP.1993
PRIOR APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP.1993
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP.1992
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSERI, 84,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
TELLECOMMUNICATION INFORMATION:
TELLEPHONE: 202-628-5197
TELLEPAX: 202-628-5197
TELLEPAX: 202-6373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US93-08528-21
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                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 50.1 Matches 214; Conservative
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                                                                                                                                                                                                                                                                                                                             STREET: 419 Sevent
CITY: Washington
STATE: D.C.
COUNTRY: USA
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419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPLISIEKKGGGGGPQP-AEPRCEINDQKWYVISSCIGSFFAPCLIW-LVYVRIYQIAKR
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RESULT 9 US-08-118-270-21

COUNTRY:

TOPOLOGY:

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                                                                                                                                                                                                                                                                Sequence 19, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
             SOFTWARE: Patentin Release #1.0, CUREBUT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                      STREET: 41, COUNTY: Washington
                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                          COUNTRY: U
ZIP: 20004
 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IGVFVLCWFPFFFSYSLGAICPKHCKVPHGLFQFFFWIGYCNSSLNPVIYTIFNQDFRRA 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFTFVLAVV 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----SNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALASVASAREVNGHSKSTGEK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLI----YKGDQGPQPRGRPQCKLNQEAWYILASSIGSFFAPCLIMILVYLRIYLIAKR 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EIYLALDVLFCTSSIVHLCAISLDRYWSITQAIEYNLKRTPRRIKAIIITVWVISAVISF 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTPRRIKCIILTVWLIAAVISL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVFGNVLVIIAVFTSRALKAPQNLFLVSIASADILVATLVIPFSLANEVNGYWYFGK-WC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FKKILCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRRILCR 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEEEEEEEEEEEECEPQAVP 316
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                                                                                                                                                                                                                     419 Seventh Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        330
                                                                                                                                                                         USA
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US 07/943,236
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                                                                                                                                                                                                                       Ν. W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSVPRTLFKFFFWFGYCNSSLNPVIYTIFNHDFRRA
                                                                             Version
                                                                                                                                                                                                                       Suite 300
                                                                              #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

STATE: I

D.C.

USA

Washington

20004

CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.,

Suite 300

AND METHODS THEREOF

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PCT-US93-08528-19
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Sequence 19, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND MINUMBER OF SEQUENCES: 348
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TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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TOPOLOGY: lir
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REFERENCE/DOCKET NUMBER: MURPHY=2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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Local Similarity 48.3%;
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Pred. No. 7.6e-58;
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Suite

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RESULT 13
US-08-196-989B-11
                                                                                                            Sequence 11, Application US/08196989B
Patent No. 5585476
GENERAL INFORMATION:
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        NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik &
                                                               APPLICANT: MacLennan, A. John
TITLE OF INVENTION: Molecular
TITLE OF INVENTION: G-Protein
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TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
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APPLICATION NUMBER: US 0:
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Keyin G.
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REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2
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Release #1.0,
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            Saliwanchik
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Coupled
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Receptors
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                                                               RESULT 14
US-08-760-936-11
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          Sequence 11, Applicat Patent No. 5856443
GENERAL INFORMATION:
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Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/08/196,989B
FILING DATE: 15-FEB-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REGISTRATION NUMBER: 35,589
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TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
APPLICANT:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CITY: Gainesville
STATE: FL
COUNTRY: US
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les 202; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
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                                                                                                                                                                                                                                                                                                                          SAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEEEE
                                                                                                                                                                                                                                                                                                                                                                                               FAPCLIMILVYVRIYQIAKRTR----
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                                              Application US/08760936
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Score 950.5; DB 1; Pred. No. 1.9e-55; 16; Mismatches 174;

Indels Length 450;

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MacLennan,

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; MOLECULE TYPE:
US-08-760-936-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 202;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 450 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,936
FILING DATE: December 6, 1996
CLASSIFICATION: 536
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NAME: PACE, DOTAN R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: MA
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CORRESPONDENCE ADDRES
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STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Galnesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: not
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                                                                                               QLTREKRFTFVLAVVIGVFVLCWFPFFFFSYSLGAICPKHCKVPHGLFQFFFWIGYCNSSL 421
                                                                                                                                 EEEEEEEECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRA 361
                                                                                                                                                                                                  PRRIKCIILTVWLIAAVISLPPLI----YKGDQGPQPRGRPQCKLNQEAWYILASSIGSF 181
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                               NPVIYTIFNQDFRRAFRRILC 442
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 NPVIYTIFNHDFRRAFKKILC 442
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3: protein
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Pred. No. 1.9e-55;
86; Mismatches 174;
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Patent No. 6518414
GENERAL INFORMATION:
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Best Local S
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ZIP: 3266
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
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TELEPAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 11:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,936
FILING DATE: 6-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/196,989
FILING DATE: 15-FEB-1994
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STRANDEDNESS: not rele
TOPOLOGY: not relevant
MOLECULE TYPE: protein
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LENGTH: 450 amino acids
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NAME: Pace, Doran R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: MA
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STATE: FL
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                                                                                                                                                                                                                                        SAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEEEE 301
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2421 N.W. 41st Street, Suite A-1
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Result
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Maximum Match 100%
Listing first 45 summaries
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2351.5
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2351.5
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1079.5
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DB seq length: 2000000000
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2378
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. /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
. /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
. /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
. /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
. /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
. /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
. /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
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   9 US-09-825-923-4
15 US-10-007-870-4
15 US-10-001-073-7
15 US-10-25-567A-42
19 US-09-825-923-2
19 US-10-001-073-8
15 US-10-001-073-2
15 US-10-001-073-2
16 US-10-001-073-2
17 US-10-001-073-2
18 US-10-001-073-4
18 US-10-001-073-4
19 US-10-001-073-4
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19 US-10-001-073-4
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                            Sequence 4, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 2, Appli
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Sequence 8, Appli
Sequence 8, Appli
Sequence 26, Appl
Sequence 26, Appl
Sequence 40, Appl
Sequence 40, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 44, Appl
                                                                                                                                                                                                                                                                                            Description
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US-09-825-923-4

Sequence 4, Application US/09825923 Patent No. US20010016338A1 GENERAL INFORMATION:

APPLICANT: Snapir, Amir APPLICANT: Heinonen, Pau APPLICANT: Alhopuro, Pia APPLICANT: Karvonen, Mat APPLICANT: Koulu, Markku APPLICANT: Pesonen, Ulla

Heinonen, Paula Alhopuro, Pia Karvonen, Matti Koulu, Markku Pesonen, Ullamari Scheinin, Mika Salonen, Jukka T

APPLICANT: APPLICANT:

Tuomainen, Tomi-Pekka

45	44	43	42	41	40	39	38	37	36	35	3 4	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
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8-661-	US-10-118-804-13	US-10-292-798-658	US-10-225-567A-102	57-031-7	0-060-		-10-054-	-10-241-	-10-054-	-10-054-6	-10-054-6162	US-10-017-161-754	US-10-224-260-20	-10-238-667-	-10-238-129-		-238-	æ		52-	-992-238-	5-930	-951-622-	-292-798	60-2	US-10-060-795B-2	25-56	36-489-	US-09-884-430-8
e 10,	e 1	e 658	e 102	e 78,	e 11,	e 2,	е 3,	e 4,	e 5,	e 4,	e 2,	75	e 20	e 10	e 10	e 36	e 4,	4.	е 4,	e 2,	e 10	Sequence 10, Appl	10	e 46	e 22	e 2, App]	e 106	8	Sequence 8, Appli

## ALIGNMENTS

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; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-923-4
Query Match 100.0%; Score 2378; DB 9; Best Local Similarity 100.0%; Pred. No. 8.7e-162; Matches 450; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                          SEQ ID NO 4
                                                                                                                                                                                                                                                                           APPLICANT: Lakka, Timo A
APPLICANT: Nyyss"nen, Kristiina
APPLICANT: Salonen, Riitta
APPLICANT: Salonen, Riitta
APPLICANT: Kauhanen, Jussi
APPLICANT: Kauhanen, Veli-Pekka
APPLICANT: Valkonen, Veli-Pekka
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: protein, and uses thereof
TITLE REFERENCE: Alpha-2B-AR variant
CURRENT FILING DATE: 2001-04-05
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR PILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
                                                           Length 450;
   0
   Gaps
   0
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Sequence 4, Application US/10077870
; Sequence 4, Application US/20030003470A1
; GENERAL INFORMATION:
; APPLICANT: Salonen, Jukka T
; TITLE OF INVENTION: Method for detecting a ris
; FILE REFERENCE: 0933-01839
; CURRENT APPLICATION NUMBER: US/10/077,870
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: FI 20010323
; PRIOR APPLICATION NUMBER: FI 20010323
; PRIOR FILING DATE: 2001-02-20
; SOFTWARE: Patentin Ver. 3.1
; SEQ ID NO 4
; SEQ ID NO 4
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-077-870-4
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Best Local Similarity
Matches 450; Conserv
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                                                              NSKRTPRRIKCTILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGS
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; TYPE: PRT
; ORGANISM: Homo sapiens
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APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 2378; DB 15; Best Local Similarity 100.0%; Pred. No. 8.7e-162; Matches 450; Conservative 0; Mismatches 0;
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Publication No. US20030113725A1
GENERAL INFORMATION:
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                                                                                       AQLTREKRETEVLAVVIGVEVLCWEPEFEFSYSLGAICPKHCKVPHGLEQEFEWIGYCNSS
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                                                                                                                                                                                                                                                                                                                      NSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGS
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           LNPVIYTIFNQDFRRAFRRILCRPWTQTAW
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: LifeSpan Biosciences
APPLICANT: Burmer, Joseph P.

APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.

TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROT
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 00/257,144
PRIOR FILING DATE: 2000-12-19
INVMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
SEQ ID NO 42
LENGTH: 450
TYPE: PRT
ORGANISM: Homo Bapiens
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US-09-825-923-2
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   APPLICANT: Snapir, APPLICANT: Heinoner APPLICANT: Alhopurc APPLICANT: Karvoner APPLICANT: Koulu, NAPPLICANT: Scheinit APPLICANT: Scheinit APPLICANT: Scheinit Salonen,
                                                                                                                               Sequence 2, Application US/09825923 Patent No. US20010016338A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 42, Application US/10225567A Publication No. US20030113798A1
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 Heinonen, Paula
Alhopuro, Pia
Karvonen, Matti
Koulu, Marku
Pesonen, Ullamari
Scheinin, Mika
Salonen, Jukka T
                                                                                                                                                                                                                                              LNPVIYTIENQDERRAFRRILCRPWTQTAW 450
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Pred. No. 3.2e-161;
1; Mismatches 1;
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Sequence 2, Application US/10077870

Publication No. US20030003470A1

GENERAL INFORMATION:
APPLICANT: Salonen, Jukka T

TITLE OF INVENTION: Method for detecting a ris
FILE REFERENCE: 0933-0183P

CURRENT APPLICATION NUMBER: US/10/077,870

CURRENT FILING DATE: 2002-05-21

PRIOR APPLICATION NUMBER: FI 20010323

PRIOR APPLICATION NUMBER: FI 20010323

PRIOR FILING DATE: 2001-02-20

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 3.1

SEQ ID NO 2
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US-09-825-923-2
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Best Local :
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APPLICANT: Valkonen, Veli-Pekka
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
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APPLICANT:
APPLICANT:
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TYPE: PRT
ORGANISM: Homo s
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                      LNPVIYTIFNQDFRRAFRRILCRPWTQTAW
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Salonen, Riitta
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Pred. No. 6.7e-160;
0; Mismatches 0;
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Sequence 8, Application US/10001073
Publication No. US20030113725A1
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Liggett, Stephen
FILE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
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; LENGTH: 447
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; ORGANISM: Homo sapiens
US-10-077-870-2

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99.3%;
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                                                                                                                                                     Score 2351.5; DB 15; Length 447; Pred. No. 6.7e-160; O; Mismatches 0; Indels 3;
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Pred. No. 6.7e-160;
0; Mismatches 0; Indels
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APPLICANT: Liggett, Stephen
APPLICANT: Liggett, Stephen
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT APPLICATION VOMBER: 2001-11-01
CURRENT APPLICATION VOMBER: 2.0
LENGTHARE: PatentIn Ver. 2.0
LENGTH: 450
TYPE: PRT
ORGANISM: Homo sapiens
US-10-001-073-27
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US-10-001-073-27
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Publication No. US20030113725A1
GENERAL INFORMATION:
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--VGAIGGQWWRRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPKHCKVPHG 406
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                                                                                    AEPLPT----QLNG---APGEPAPA-GPRDTDALDLEES---
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Sequence 26, Application US/10001073

Publication No. US20030113725A1

GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
ITILS OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073

CURRENT FILING DATE: 2001-11-01

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 26

LENGTH: 450
TYPE: PRT
ORGANISM: Homo sapiens

US-10-001-073-26
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US-10-001-073-26
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                                                               Sequence 40, Application US/10225567A Publication No. US20030113798A1 GENERAL INFORMATION:
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   APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
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Brown, Joseph P.
Burmer, Glenna C.
Roush, Christine L
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Sequence 44, Application US/1025567A

Publication No. US20030113798A1

GENERAL INFORMATION:

APPLICANT: LifeSpan Biosciences

APPLICANT: Brown, Joseph P.

APPLICANT: Burmer, Glenna C.

APPLICANT: Roush, Christine L.

TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTELICATION NUMBER: US/10/225,567A

CURRENT APPLICATION NUMBER: US/10/225,567A
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; ORGANISM: Homo US-10-225-567A-44
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FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR PILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOPTWARE: Patentin version 3.1
SEQ ID NO 40
                                  SOFTWARE: PatentIn version 3.1
SEQ ID NO 44
LENGTH: 461
TYPE: PRT
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Best Local !
                                                                                                         PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SASGLP--RRRAGAGGQNLEKRETEVLAVVIGVEVVCWEPEPETYTLTAV---GCSVERT 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                               LFKFFFWFGYCNSSLNPVIYTIFNHDFRRAFKKILCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LFQFFFWIGYCNSSLNFVIYTIFNQDFRRAFRRILCR 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAIGGQWWRRRAQL---TREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPKHCKVPHG 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDEAEE----EEEEEEEEEECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGV 349
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                 sapiens
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52.7%;
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                                                                                                                                                                                                                        ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                               443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GRRLQGRGR 351
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Sequence 46, Application US/10001073

Publication No. US20030113725A1

GENERAL INFORMATION:

APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION: Alpha-2-adrenergic receptor polymorphisms
CURRENT FILING DATE: 2001-11-01

CURRENT FILING DATE: 2001-11-01

SOFTMARE: Patentin Ver. 2.0

SEQ ID NO 46

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US-10-001-073-46
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Best Local Similarity 52.2
Matches 240; Conservative
                                                                                                                                                                                                                                                                                                                                                               Local
                                                        166 RRVKATIVAVWLÍSAVÍSFÞÞÍVSLÝR----QÞDGAAYÞQCGÍNDETWYÍÍSSCÍGSFF
                                                                             127 RRIKCIILTVWLIAAVISLPPLI--YKGDQGPQPRGR--PQCKLNQEAWYILASSIGSFF 182
                                                                                                                                                                                106
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                                                                                                                                                                                                                       414 PGPLEKFEFWIGYCNSSLNPVIYTVENQDERPSFKHILER 453
                                                                                                                                                                                                                                                                                                          h
Similarity 53.8; Score 1071; DB 15; Length 458;
Similarity 53.8; Pred. No. 1.7e-68;
41; Conservative 44; Mismatches 107; Indels 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              344_LLGRGVGAIGGQWWRRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPKHCKV 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        404
                                                                                                                                          PPSLANELMAYWYFGQVWCGVYLALDVLFCTSSIVHLCAISLDRYWSVTQAVEYNLKRTP
                                                                                                                                                              PFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTP 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           285 KEGVCGASPEDEAEEEEEEEEEEEEEEEPQAVPVSPASACSPPLQQPQGSRVLATLRG-QV 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 PTTENGLGAAAGEAR-----TGTARPREPTWSRTRAAQRERGGAPGPLRRGGRRRAGA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221 ĀPĊLĪMGLVYARĪYRVĀKRRTR-------TLSEKRAPVGPDGĀS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 RŘVKATÍVAVMLÍSAVIŚFÞÞĽVSLÝR----QÞDGAAYÞQCGLNDETWYÍĽSŚCIGŚFF 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 PFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTP 126
||||||||: ||| ||| || 126
106 PFSLANELMAYWYFGQVWCGVYLALDVLFCTSSIVHLCAISLDRYWSVTQAVEYNLKRTP 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGĠAGĠĄ-----DGQGAGPĠÀAQSGALTÁSRSP--GPGGRLSRÁSSRSVEF 354
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52.2%; Pred. No. 5.1e
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                                                                                                                                          165
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| Sequence 44, Application No. US20030113725A1
| GRNERAL INFORMATION: APPLICANT: Liggett, Stephen APPLICANT: Liggett, Stephen FILE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms CURRENT APPLICATION NUMBER: US/10/001,073
| CURRENT APPLICATION NUMBER: US/10/001,073
| CURRENT APPLICATION NUMBER: US/10/001,073
| NUMBER OF SEQ ID NOS: 53
| SEQ ID NO 44
| LENGTH: 462
| TYPE: PRT | ORGANIGM: Homo sapiens
| US-10-001-073-44
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US-10-001-073-44
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Local Similarity 45.0%; Score 1070; DB 15; Length 462;
Local Similarity 53.6%; Pred. No. 2.le-68;
les 241; Conservative 45; Mismatches 110; Indels 54
414 IGYCNSSLNPVIYTIFNQDFRRAFRRILCR 443
                           366 SVCRŘKVÁQ-AREKRÉTEVLÁVVMGVEVLCWÉPÉFÉTYSLYGICREACQVÉGELEKÉFÉW
                                                      354 GQWWRRRAQLTREKRETEVLAVVIGVEVLCWEPEFESYSLGAICPKHCKVPHGLFQFFFW
                                                                                                                                              295 DEAHEEBEEEEEEEEEEEPOAVPVSPASACSPPLOOPOGSRVLATLRG-OVLLGRGVGAIG 353
                                                                                                                                                                                       268 ÁGÁGÉ-NGHCAPPPADVÉPDÉSSAAAERRRRR-----GÁLRRGGRRRAGAEGGAGGÁ--- 318
                                                                                                                                                                                                                             241 ASARBVNGH---SKSTGEKBEGETPEDTGTRALPPSWAALPNSGQ---GQKEGVCGASPE 294
                                                                                                                                                                                                                                                                                                             183 APCLIMILVYLKIYLIAKKSNR---RGPRAKGGPGQGESKQPRPDHGGALASAKLPALASV 240
                                                                                                                                                                                                                                                                                                                                                          166 RŘVKATÍVAVWLÍSÁVÍSFÞÞLVSLYR-----ÓÞDGAAYÞÓCGLNDÈTWYILSSCIÓSFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106
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                                                                                                                                                                                                                                                                        APĊĹĬMGĹVŶAKĬŶRVÅKRRTŘTLSEKŘÁPVĠĎ---DGASĎTTENĠ-----LGAA 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ÁGÁGÉ-NGHCAPPPADVÉPDÉSSAAAERRRŘR----GÁLRRGGRRRAGAEGGAGGÁDGO 321
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CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: 09/238977
PRIOR FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: 08/474892
PRIOR FILING DATE: 1995-06-07
PRIOR PPLICATION NUMBER: 07/973588
PRIOR PILING DATE: 1992-11-09
PRIOR PILING DATE: 1992-11-09
PRIOR PILING DATE: 1989-11-20
PRIOR FILING DATE: 1989-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 07/273373
PRIOR FILING DATE: 1988-11-18.
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN Ver: 2.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/10060795B Publication No. US20030040022A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -10-060-795B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Civelli Olivier
APPLICANT: Bunzow, James R.
APPLICANT: Grandy, David K.
APPLICANT: Machida, Curtis A.
TITLE OF INVENTION: Dopamine Receptors and
FILE REFERENCE: 90-1092-CCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
                                                                          228
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285
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                                                                                                                                                                                                                                                              242 SAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEEEE 301
                                                                                                                                                                                                                                                                                                                                                                                                                 126 PRRIKCIILTVWLIAAVISLPPLI----YKGDQGPQPRGRPQCKLNQEAWYILASSIGSF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                          87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 IPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     σ
                             NPVIYTIFNQDFRRAFRRILCR 443
                                                                          RVPREKRETEVLAVVIGMEVVCWEPEEETYTLTAV--
                                                                                                 QLTREKRFTFVLAVVIGVFVLCWFPFFFFSYSLGAICPKHCKVPHGLFQFFFWIGYCNSSL 421
                                                                                                                                                                                     EEEEEEEECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRA 361
                                                                                                                                                                                                                                                                                                                                      FAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALASVA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPFSLANEVMQYWYFGKTWCEIYLALDVLFCTSSIVHLCAISLQRYWSITQAIEYNLKRT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYSLOVTLTLVCLAGLIMLLTVFGNVLVIIAVFTSRALKAPONLFIVSLASADILVATLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYSVQATAAIAAAITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADILVATLI 65
NPVIYTLENHDERRAFWKILCR 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 959; DB 15;
Pred. No. 1.1e-60;
42; Mismatches 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 166;
                                                                                                                                                  ----RRT 227
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RESULT 15

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Patent No. Usac.
Patent INFORMATION:
                                                                                                                                                                                                                                                                                                                                             Best Local Similarity Matches 164; Conserv
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 84, Application US/09782980 Patent No. US20020072089A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/276,400 PRIOR FILING DATE: 1999-03-25 PRIOR APPLICATION NUMBER: 60/117,580 PRIOR FILING DATE: 1999-01-27 PRIOR APPLICATION NUMBER: 09/014,195 PRIOR FILING DATE: 1998-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 176
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/782,980
CURRENT FILLING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: PCT/US00/02125
PRIOR FILING DATE: 2000-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Khodadoust, Mehran M. APPLICANT: MacBeth, Kyle J. APPLICANT: Busfield, Samantha J. APPLICANT: Busfield, Samantha J. APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 60
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/448,076 PRIOR FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL ITAL
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 09/049,799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1998-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 09/087,121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 09/561,810 FILING DATE: 2000-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1998-04-21 APPLICATION NUMBER: 09/561,381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/063,950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 09/086,892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 09/014,348 FILING DATE: 1998-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/672,721
293
                                        196
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INVENTION: NOVEL ITALY, LOR-2, STRIFE, TRASH, BDSF, LRSG,
INVENTION: STMST PROTEIN AND NUCLEIC ACID MOLECULES AND (
                                                                                                                                                                                                                                                          ALVLSVIIVLTIIGNILVILSVFTYKPLRIVQNFFIVSLAVADLTVALLVLPENVAYSIL 172
FVATRRRLRERARANKLNTIÁLKSTELEÞMANSSÞVAASNSGSKSRLLASWLCCGRDRAQ 352
                                        YL----
                                                                                  VWLLSLLISSPELIGWNDWPDEFTSATPCELTSQRGYVIYSSLGSFFIPLAIMTIVYIEI
                                                                                                                           VWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGSFFAPCLIMILVYLRI 195
                                                                                                                                                                                                              GYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALBYNSKRTPRRIKCIILT 135
                                                                                                                                                                        GRWEFGIHLCKLWLTCDVLCCTSSILNLCAIALDRYWAITDPINYAQKRTVGRVLLLISG 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Holtzman, Douglas A.
                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                72; Mismatches 181;
                                                                                                                                                                                                                                                                                                                                                                    Score 651; DB 9;
Pred. No. 2.2e-38;
                                        IAKRSNRRGPRAKGGPG---
                                                                                                                                                                                                                                                                                                                                                                                      Length 601;
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Search completed: February 6, 2004, 18:22:04 Job time : 32.1003 secs	584 TIPNLDYRRAFKELL 598	427 TIENQDERRAFRRIL 441	526 RAARTIGIIMGVEVICWLEPERLMYVILEPECOTCCPTNKEKNETTWILGYTNGGI MENTY	368 RETEVLAVVIGVEVLCWEPEFESYSIGAICPKHCKVDHCTEO BEEFING	467 KGC-IQVCVTQADEQTSLKLTPPQSSTGVAAVSVTPLQKKTSGVNQPIEEKQKISLSKER 525	308 EECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAOLTREK 367	*13 KGGKKSQSSSTCEPHGEQQLLPAGGDGSSCQPGGGHSGGGKSDAEISTESGSDP 466	13 CONTRACTOR OF THE PROPERTY	253 TGEKEEGETDETTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	353 FATEMIQNDQESISSETHQEODSSKAGPHRNSDDOODSTRIKK UNGESKS 252	215QGESKQPRPDHGGALASAKLDALAGYAGADTINGTON

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq
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   Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution.
Score
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length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       283308 seqs, 96168682 residues
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2378
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1: pir1:*
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4: pir4:*
 MDHQDPYSVQATAAIAAAIT.....QDFRRAFRRILCRPWTQTAW
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 GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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## ALIGNMENTS

RESULT 1
AJ723
AJ723
AJ723
AJ723
AJ723
AJ724
ALPha-ZB-adrenergic receptor - human
Alpha-ZB-adrenergic receptor - human
Alpha-ZB-adrenergic receptor
CJSpecies: Homo sapiens (man)
CJSpecies: Homo sapiens (man)
CJSpecies: L3723; 139407; S14308; A36158
CJAccession: A3723; 139407; S14308; A36158
R;Weinshank, R.L.; Zgombick, J.M.; Macchi, M.; Adham, N.; Lichtblau, H.; Branchek, T.A.;
Mol. Pharmacol. 38, 681-688, 1990
A;Title: Cloning, expression, and pharmacological characterization of a human alpha-2B-ac
A;Reference number: A37223; MUID:91042469; PMID:2172775
A;Accession: A37223

alpha-1-adrenergic Query Match alpha-1-adrenergic Query Match dopamine receptor Best Local Similarity			alpha-2 adrenergic A; Status: preliminary alpha-2-adrenergic A; Residues: 56-185 <chh> alpha-2-adrenocept A; Cross-references: GB:X alpha-2-adrenergic A; Note: this translattion alpha-2-adrenergic R; Chang, A.C.; Ho, T.F.;</chh>		ted by chance to have a  A; Residues: nucleic actor in the result being printed, of the result being printed, of the result being printed, of the result being printed, or a R; Lomasney, J.W.; Loren Proc. Natl. Acad. Sci. 1  A; Title: Expansion of t. A; Reference number: 139  A; Reference number: 139  A; Status: preliminary A; Status: preliminary A; Molecule type: DNA A; M	A CACCESTON AS A CACC
Query Match 99.7%; Score 2370; DB 2; Length 450; Best Local Similarity 99.6%; Pred. No. 3.3e-154; Marches 448: Conservative 1: Mismatches 1: Indels 0: Gaos 0:	1; ADRA2L1; ADRA2RL1 20539; OMIM:104260 rhodopsin pled receptor; glycoprotein; transme	Biochem. Biophys. Res. Commun. 172, 817-823, 1990 A;Title: In vitro amplification by polymerase chain reaction of a partial gene encoding t A;Reference number: A36158; MUID:91054503; PMID:2173582 A;Accession: A36158 A;Accession: A36158 A;Molecule type: DNA A;Residues: 95-361, 'QL', 364-389 <cha> A;Cross-references: GB:M38742; NID:g177867; PIDN:AAA62823.1; PID:g177868</cha>	A; Status: preliminary A; Molecule type: DNA A;Residues: 56-185 <chh> A;Residues: 56-185 <chh> A;Cross-references: GB:X59684; NID:928635 A;Note: this translation is not annotated in GenBank entry HSALPH218, release 111.0 R;Chang, A.C.; Ho, T.F.; Chang, N.C.</chh></chh>	A;Cross-references: GB:M34041; NID:g178197; PIDN:AAA51666.1; PID:g178198 A;Cross-references: GB:M34041; NID:g178197; PIDN:AAA51666.1; PID:g178198 R;Chhajlani, V.; Rangel, N.; Uhlen, S.; Wikberg, J.E.S. FEBS Lett. 280, 241-244, 1991 A;Title: Identification of an additional gene belonging to the alpha(2) adrenergic recept A;Title: Identification of an additional gene belonging to the alpha(2) adrenergic recept A;Reference number: S14308; MUID:91192139; PMID:1849485 A;Accession: S14308	A; No lecule type: DNA A; No lecule type: DNA A; Residues: 1-450 <wei> R; Lonessney, J. W.; Lorenz, W.; Allen, L.F.; King, K.; Regan, J.W.; Yang-Feng, T.L.; Caron, Proc. Natl. Acad. Sci. U.S.A. 87, 5094-5098, 1990 A; Title: Expansion of the alpha 2-adrenergic receptor family: cloning and characterizatic A; Reference number: 139407; MUID:90311349; PMID:2164221 A; Accession: 139407 A; Status: preliminary A; Molecule type: DNA A; Molecule</wei>	

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alpha-2B-adrenergic receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 13-Aug-1999
C:Accession: 151883
R;Le Jossec, M.; Cloix, J.F.; Pecquery, R.; Giudicelli, Y.; Dausse, J.P.
Am. J. Hypertens. 8, 177-182, 1995
A;Fittle: Differential sodium regulation between salt-sensitive and salt-resist.
A;Reference number: I51883; MUID:95275492; PMID:7755946
A;Accession: 151883
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-448 <RES
A;Cross-references: EMBL:X74400; NID:g840862; PIDN:CAA52411.1; PID:g940816
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor
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                           FFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALAS. 239
VASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEE
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83.8%; Pred. No. 6.5e-128;
ative 24; Mismatches 45;
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C.Species: Rattus norvegicus (Norway rat)
C.Species: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
C.Accession: A35642
R.Zeng, D.; Harrison, J.K.; D'Angelo, D.D.; Barber, C.M.; Tucker, A.L.; Lu, Z.;
Proc. Natl. Acad. Sci. U.S.A. 87, 3102-3106, 1990
A.Title: Molecular characterization of a rat alpha-2B-adrenergic receptor.
A.FReference number: A35642; MUID:30222177; pMID:2158103
A.Accession: A15642
A.Molecule type: mRNA
A.Residues: 1-453 <ZEN>
A.Coss-references: GB:M32061; NID:g202589; PIDN:AAA40635.1; PID:g202590
C.Superfamily: vertebrate rhodopsin
C.Superfamily: vertebrate rhodopsin
C.Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
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                                                                                                  RTQLSREKRFTFVLAVVIGVFVVCWFPFFFSYSLGAICPQHCKVPHGLFQFFFWIGYCNS
                                                                                                                    RAQLTREKRFTFVLAVVIGVEVLCWFPFFFSYSLGAICPKHCKVPHGLFQFFFWIGYCNS
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Similarity 83.8%; Score 1981; DB 2;
Similarity 83.8%; Pred. No. 1.1e-127;
78; Conservative 24; Mismatches 45;
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9 밁 5 В ş 밁 ş 맑 á

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A;Molecule type: DNA
A;Residues: 6-228,231-455 < CHR>
A;Residues: 6-228,231-455 < CHR>
A;Cross-references: GB:L00979; NID:g191547; PIDN:AAA37131.1; PID:g191548
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
F;18-43/Domain: transmembrane #status predicted <TM1>
F;55-81/Domain: transmembrane #status predicted <TM3>
F;90-115/Domain: transmembrane #status predicted <TM4>
F;173-199/Domain: transmembrane #status predicted <TM5>
F;131-199/Domain: transmembrane #status predicted <TM6>
F;177-402/Domain: transmembrane #status predicted <TM6>
F;377-402/Domain: transmembrane #status predicted <TM7>
                                    RESULT 5
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A;Note: the authors translated the codon CCA for residue 161 as Phe, ACT R;Chruscinski, A.J.; Link, R.E.; Daunt, D.A.; Barsh, G.S.; Kobilka, B.K. Biochem. Biophys. Res. Commun. 186, 1280-1287, 1992
A;Title: Cloning and expression of the mouse homolog of the human alpha2-A;Reference number: JH0693; MUID:92378586; PMID:1354956
A;Accession: JH0693
alpha 2-adrenergic
C;Species: Rattus :
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A;Molecule type: DNA
A;Residues: 1-455 <CHE>
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C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 13-Aug-1999
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Best Local Similarity
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                                                                                                                                                                                                                      RRRAQLTREKRETFVLAVVIGVFVLCWFPFFFSYSLGAICPKHCKVPHGLFQFFFWIGYC
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                                                                                                                                                                                                                                                                                                                                                     SPLSSVGEANGHPKPPREKEEGETPEDPEARALPPNWSALPRSVQDQKKGTSGATAEKGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGESKQPRPD--HGGALASAKLPALA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MDHQDPYSVQATAAIAAAITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADIL
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                                                                                                                    NSSLNPVIYTIFNQDFRRAFRRILCRQWTQTGW
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вp.
  receptor,
sp. (rat)
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                Langerhans
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                    rat
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A;Cross-references: GB:M62372; NID:g206615; PIDN:AAA42034.1; PID:g206616 C;Superfamily: vertebrate rhodopsin C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                   alpha-2-adrenergic receptor (clone RG10) C;Species: Rattus norvegicus (Norway rat) C;Date: 06-Dec-1991 #sequence_revision 03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Status: preliminary; translated from GB/1
A, Molecule type: mENA
A, Residues: 1-276 < RES>
A, Cross-references: GB:S67316; NID:9456949
C, Superfamily: vertebrate rhodopsin
C; Keywords: neurotransmitter receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Wang, S.Y.; Pilkey, D.T.
Diabetes 43, 127-136, 1994
A;Title: Identification in islets of Langerhans of a new A;Reference number: IS3161; MUID:94085695; PMID:8262309 A;Accession: IS3161
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A; Residues: 1-450 < LAN>
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                                                                                                                                                                                                           Query Match
Best Local
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                                                                                                                                                                                                             Similarity
                      PRRIKCIILTVWLIAAVISLPPLI---YKGDQGPQPRGRPQCKLNQEAWYILASSIGSFF 182
                                                                               IPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRT
                                                                                                                                              PYSVQATAAIAAAITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADILVATLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTSSIVHLCAISLDRYWAVSRALEYNSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFTFVLA 374
                                                                                                                           PYSLOVILILVCLAGLIMLFTVFGNVLVITAVFTSRALKAPONLFLVSLASADILVATLV
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PRRIKAIIVTVWVISAVISFPPLISIEKKGAGGGQQPAEPSCKINDQKWYVISSSIGSFF
                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                           48.3%;
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                                                                                                                                                                                          ; Score 1148.5; DB
; Pred. No. 5.4e-71;
51; Mismatches 96
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A;Cross-references: GB:M99377; NID:g191882; PIDN:AAA37213.1; PID:g191883
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in antagonist binding.
A;Reference number: I49480; MUID:92342131; PMID:1353249
A;Accession: I49481
                                 396 ICPKHCKVPHGLFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCR 443
                                                                                 342 PGASGSGHGEEŘĠĠĠÁKASRW---ŘGRONRĚKŘĖŤĚVĽÁVVÍĠVĚVVCWEPĚĚFTYTĽIÁ
                                                                                                                                                                                                                                                                                                                                        238 ASVASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEA
                                                                                                                                                                                                                                                                                                                                                                                                                                 183 APCLIMILUYLRIYLIAKR-----SNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPAL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               399 KHCKVPHGLFOFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCR 443
                                                                                                                                                                                ALDLÉESSSSÉHAERPPGPRRPDRGPRÁKGKTRÁSQVKÞGDSLÞR-----RGPGAAG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             342 PGASGSÓÓGEEŔAGGAKASRWŔGRQNŔĖKŔĖTĖVĹÁVVÍĠVĖVVĆWĖĖĖĖĖTYTĹLÁV-- 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 -----GQWWRR------RAQLTREKRETEVLAVVIGVEVLCWEEEFESYSLGAICE 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 48.0%; Score 1141.5; DB 2; Similarity 52.4%; Pred. No. 1.6e-70; 45; Conservative 42; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                             APĊĹĬŇĬĹVŶVŔĬŶQĬÁKĬRTRVÞPSŘŘĞÞDÁCSAÞÞGĞADRRÞ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRRÍKAÍÍVTVWVÍSÁVÍSFÞÞLÍSIEKKGAGGGÓQÞABÞSCKINDQKWYVISSSÍGSFÞ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 EPLPT-----QLNG---APGE-----PAPT--
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                                                                                                                                                                                                                                                                                     NGLG----PERGAGĖ--TGAEAEĖ----LĖTQLNGAPGEPAPAGERDGD 289
                                                                                                                  -RGVGAIGGOWWRRRAQLTREKRETEVLAVVIGVEVLCWEPPEFESYSLGA 395
                                                                                                                                                                                                                                --PQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLG 346
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                                                                                 398
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A;Cross-references: GDB:120538; OMIM:104210
A;Map position: 10q25-10q25
A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Molecule type: DNA
A; Residues: 1-103, 'T', 105-156, 'C', 158-367, 'L', 369-450 < KOB>
A; Cross-references: GB: M.18415; NID: 9178191; PIDN: AAA51664.1; PID: 9178192
A; Note: the authors translated the codon TgT for residue 157 as Val, and R; Chhajlani, V; Rangel, N; Uhlen, S; Wikberg, JE.S.
A; Title: 180, 241-244, 1991
A; Reference number: S14108; MUID: 91192139; PMID: 1849485
A; Accession: S14311
A; Residues: T7-123, 'P', 125-209 < CHH>
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alpha-An-adrenergic receptor - human

NAlternate names: alpha-2C10-adrenergic receptor

C;Species: Homo sapiens (man)

C;Date: 22-Jan-1993 #sequence revision 22-Jan-1993 #text_change 29-Oct-1999

C;Accession: A34169; A40132; S14311

R;Fraser, C.M.; Arakawa, S.; McCombie, W.R.; Venter, J.C.

J. Biol. Chem. 264, 11754-11761, 1989

A;Title: Cloning, sequence analysis, and permanent expression of a human algorithm of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contr
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R; Kobilka, B.K.; Matsui, H.; Kobilka, T.S.; Yang-Feng, T.L.; Francke, U.; Caron, M.G.,
A; Title: Cloning, sequencing, and expression of the gene coding for the human platelet
A; Accession: A40132; MUID:88042789; PMID:2823383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: A34169; MUID:89308571; PMID:2568356
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A34169
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  299 SDHÅERPPGPRRPERGPRGKGKARÅSQVKÞGDSLRGAGRGRRGS-
                                                                                      294
                                                                                                             266 AEPLPT-----QLNG---APGEPAPA-GPRDTDALDLEES
                                                                                                                                         234 LPALASVASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASP 293
                                                                                                                                                                                                                                                                                                182
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                                                                                                                                                                                                                                                                                                                                          126 PRRIKCIILTVWLIAAVISLPPLI----YKGDQGPQPRGRPQCKLNQEAWYILASSIGSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242;
                                                                                                                                                                                                                                                                                                                                                                                                                                       66 IPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRT 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 53.0
42; Conservative
                                                                                                                                                                                                 PAPČĽÍMIĽVÝVŘÍÝQÍÁKKRTRVPPSŘŘĠÞDÁVAAPPGGTERRĖNGLGPERSAGPGGÁB
                                                                                                                                                                                                                                              FAPCLIMILVYLRIYLIAKR-----SNRRGPRAKGGPGQGESKQPR---PDHGGALASAK 233
                                                                                                                                                                                                                                                                                                                                                                                                        I PFSLÁNEVMGYMY FGKAMCEI YLALDVÍ FCTSSÍ VHÍ CÁ Í SÍÐR YMSI TQÁ I EYNLKRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.3%; Score 1124.5; DB 2; 53.0%; Pred. No. 2.3e-69; tive 52; Mismatches 104;
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Francke, U.; Caron, M.G., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59;
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A; Molecule type: DNA A; Residues: 1-450 < RES>

Query Match Best Local (

Local

245;

A/Status: preliminary; translated from

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295

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В Ś 밁 Ş 밁 Ś B Ś 8 Ś 밁 ş

290 298

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147

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alpha 2-adrenoceptor - cuckoo wrasse
(Species: Labrus ossifagus (cuckoo wrasse)
(C; Species: Labrus ossifagus (cuckoo wrasse)
C; Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_c
C; Accession: I50829
R; Svensson, S.P.; Bailey, T.J.; Pepperl, D.J.; Grundstrom,
R; Svensson, S.P.; Bailey, T.J.; Pepperl, D.J.; Grundstrom,
Br. J. Pharmacol. 110, 54-60, 1993
A; Title: Cloning and expression of a fish a2-adrenoceptor.
A; Reference number: I50829; MUID:94035926; PMID:7693288
                                                                                                                              RESULT 10
I50829
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R;Guyer, C.A.; Horstman, D.A.; Wilson, A.L.; Clark, J.D.; Cragoe Jr., J. Biol. Chem. 265, 17307-17317, 1990
A;Title: Cloning, sequencing, and expression of the gene encoding the A;Reference number: A38316; MUID:91009167; PMID:2170371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
A38316
A18316
C:Species: Sus scrofs domestica (domestic pig)
C:Date: 22-Uan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
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A;Molecule type: DNA
A;Residues: 1-450 <GUY>
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Best Local S
Matches 241
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                                                                                                                                                                                                                                                                      GRGVGAIGGQWWRRRAQLTREKRPTFVLAVVIGVFVLCWFPFFFSYSLGAICFKHCKVPH
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52.6%;
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; Pred. No. 5.9e.
46; Mismatches
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                                                Ala-Uotila,
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                                                  Scheinin
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                 Matches
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F;34-59/Domain: hydrophobic <HII>F;710-96/Domain: hydrophobic <HII>F;106-131/Domain: hydrophobic <III>F;106-175/Domain: hydrophobic <HIV>F;150-175/Domain: hydrophobic <HIV>F;153-218/Domain: hydrophobic <HVI>F;375-400/Domain: hydrophobic <HVI>F;405-430/Domain: hydrophobic <HVI>F;405-430/Domain: hydrophobic <HVI>F;405-430/Domain: hydrophobic <HVI
                                                                                                                                                                                                                                                                                                                 R;Chalberg, S.C.; Duda, T.; Rhine, J.A.; Sh
Mol. Cell. Biochem. 97, 161-172, 1990
A;Title: Molecular cloning, sequencing and
A;Reference number: JH0190; MUID:91125329;
                                                                                                                                                                                                                             A; Experimental source: brain C; Comment: Alpha-2-adrenergic receptor is a
                                                                                                                                                                                                                                                                                                                                                                                                                       alpha-2-adrenergic receptor - rat
C; Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: I50829
A;Status: preliminary; translated from GB/EMBI
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-432 <SVE>
A;Cross-references: EMBL:U07743; NID:g467287;
C;Superfamily: Vertebrate rhodopsin
                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-450 < CHA>
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                                                                                                                                                                                          ;Superfamily: vertebrate rhodopsin;Keywords: G protein-coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                       ;Species: Rattus norvegicus (Norway ra;Date: 31-Dec-1991 #sequence_revision
                                  Query Match
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al Similarity
237; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YCNSSLNPVIYTIFNQDFRRAFRRILCRPWTQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IAEKKVSQAREKRFTFVLAVVMGVFVVCWFPFFFSYSLHAVCRDYCKIPDTLFK-FFWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L-----TREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPKHCKVPHGLFQFFFWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEEEEEECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAQ 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGLNKANSPCHGDRENGHC-----QCPPT-----PSQRTVTIG-QQTDDADMDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGHSKST----GEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEEEEE 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGSFFAPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTP 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMILVYIRIYQVAKTRTR
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                45.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62;
                  Score 1091.5;
Pred. No. 4.1e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1106.5; DB Pred. No. 3.7e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          31-Dec-1991 #text_change 16-Feb-1997
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                  No. 4.1e-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SMSGKEPRPD
                                                                                                                                                                                                                                                                                                                   expression of PMID:2177834
                                                                                                                                                                                                                              predominant catecholamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIDN:AAA17386.1;
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                                    450;
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Conservative

49;

Mismatches

Indels

85;

Gaps

12;

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Db 147 RRITANTICHY III PRIL - YKOGOGOPORANGOLISH III III PRISKRY 128  Db 23 AGCHINILIYA I III PRIL - YKOGOGOPORANGOLISH III III PRISKRY 128  Db 23 AGCHINILIYA I III PRIL - YKOGOGOPORANGOLISH III III III PRISKRY 128  Db 23 AGCHINILIYA I III III PRIL - YKOGOGOPORANGOLISH I III III III III III III III III II	Oy  6 PYSUQATAAIAAAITFLILFTIFGNALVILAVLTSR8LRAPONLFLUSLAAADILVATLI 65  OY  66 IPFSLANELLGYMYERRTWCEVYLALDVLFCTSSALKAAPONLFLUSLAAADILVATLI 65  B7 IPFSLANELLGYMYERRTWCEVYLALDVLFCTSSIVHLCALSADILVATLV 66  OY  126 PRRIKCT
DO 234 EDBLAEEREEREEREEREEROPHY PRODUCTS	8-09-692-077 <b>d-7.</b> Fpr

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RESULT 15
A31237
alpha-2C-adrenergic receptor - human
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 13-Aug-1999
C;Accession: A31237; S14309; S14310
R;Regan, J.W.; Kobilka, T.S.; Yang-Feng, T.L.; Caron, M.G.; Lefkowitz, R.J.;
Proc. Natl. Acad. Sci. U.S.A. 85, 6301-6305, 1988
A;Title: Cloning and expression of a human kidney cDNA for an alpha-2-adrent
A;Reference number: A31237; MUID:88320430; PMID:2842764
A;Accession: A31237
A;Accession: A31237
A;Molecule type: mRNA
A;Residues: 1-461 <REG>
A;Crose-references: GB:J03653; NID:g178193; PIDN:AAA35513.1; PID:g178194
A;Chhajlani, V.; Rangel, N.; Uhlen, S.; Wikberg, J.E.S.
FEBS Lett. 280, 241-244, 1991
A;Title: Identification of an additional gene belonging to the alpha(2) adrenergic recep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Chang, Y.H.; Chang, N.C.; Chen, W.M.; Chang, A.C.
Blochem. Mol. Biol. Int. 29, 467-474, 1993
A;Title: Molecular characterization of a murine homologue of alpha 2C4 adrenoceptor subt A;Reference number: A48392; MUID:93250567; PMID:8387367
A;Accession: A48392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alpha 2C4 adrenoceptor subtype - mouse
N;Alternate names: alpha 2C4 isoceptor
C;Species: Mus musculus (house mouse)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C;Accession: A48392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Note: sequence extracted from NCBI backbone (NCBIN:131475, NCBIP:131476) C;Superfamily: vertebrate rhodopsin C;Keywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Status: preliminary
A,Molecule type: nucleic acid
A,Residues: 1-458 <CHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLGRGVGAIGGQWWRRRAQLTREKRETFVLAVVIGVFVLCWFPFFFESYSLGAICPKHCKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VASAREVNGH----SKSTGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRVKATIVAVWLISAVISFPPLVSFYR----RPDVAAYPQCGLNDETWYILSSCIGSFFAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YSVQATAAIAAAITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAAADILVATLII 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLSRRRARSSVCRRKVAQ-AREKRFTFVLAVVMGVFVLCWFPFFFSYSLYGICREACQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLIMILVYLRIYLIAK-----RSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALBYNSKRTP
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ilarity 51.3%;
Conservative 4
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Pred. No. 3e-66;
17; Mismatches
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                                                                                                                                                                                                                               Lefkowitz, R.J.; Kobilka,
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                                                                                                                                                                                   alpha-2-adrenergic recepto
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 95-223 < CHH>
A;Accession: $14310
A;Molecule type: DNA
A;Residues: 95-223 < CH2>
C;Genetics:
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A;Cross-references: GDB:120540; OMIM:104250
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C; Superfamily: vertebrate rhodopsin
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GO; GO:0005887; C:integral to plasma membrane; TAS,
GO; GO:0004938; F:alpha2-adrenergic receptor activity; TAS.
GO; GO:0007267; P:cell-cell signaling; TAS.
GO; GO:0007266; P:C-protein coupled receptor protein signalin.
InterPro; IPR000276; GPCR_Rhodpsn.
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                               61
                                                                                                                                                                                                                                                             Similarity
VATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEY 120
                                                                  MDHODPYSVOATAAIAAAITFLILFTIFGNALVILAVLTSRSLRAPONLFLVSLAAADIL
                                                                                                         MDHQDPYSVQATAAIAAAITFLILFTIFGNALVILAVLTSRSLRAPQNLPLVSLAAADIL
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450
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                                                                                                                                                                                                                                                                                                                                                        MW,
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Pred. No. 2.8e-128;
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5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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CYTOPLASMIC (
4 (POTENTIAL)
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IMPLICATED IN CATECHOL AGONIST BINDING
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IMPLICATED IN LIGAND BINDING
SIMILARITY).
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2L -> HV (IN REF. 1 AND 2).
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EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL)
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3 (POTENTIAL).
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InterPro; IPR000276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GFCRRHODOPSN.

PROSITE; PS00237; G PROTEIN_RECEP_F1_1; 1.

PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

G-protein_coupled_receptor; Transmembrane; Multigene family;
                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it is by non-profit institutions as long as its content is in no was entitied and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Svensson S.P., Bailey T.J., Porter A.C., Richman J.G., Ruthercologous expression of the cloned guinea pig alpha; and alpha 2C adrenoceptor subtypes. Radioligand binding functional coupling to a CAMP-responsive reporter gene. Biochem. Pharmacol. 51:291-300(1996).

-i- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CINDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE
                                                                                                                                                                                                   EMBL; U25723; AAA67075.1;
HSSP; P29274; 1MMH.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae;
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L-NOV-1997 (Rel. 35, Last sequence update)
L-NOV-2001 (Rel. 40, Last annotation update)
Lpha-2B adrenergic receptor (Alpha-2B adrenoceptor).
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SUBCELULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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EXTRACELLULAR (POTENTIAL).

1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

Eukaryota; Metazoa; Mammalia; Eutheria; NCBI\_TaxID=10116;

Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

SEQUENCE FROM N.A.

DOMAIN

Query Match Best Local & Matches

399;

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PATAB RAT PRT; 4
P1932B; Q63021;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Alpha-2B adrenergic receptor (Alpha-2B
ADRA2B.
Rattus norvegicus (Rat)
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Pred. No. 4.2e-111;
5; Mismatches 33;
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IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
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Pfam; PF00001; 7tm 1; 1.

PRINTS; PR000237; GECRRHODPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1 1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1 2; 1.

G-protein_coupled_receptor; Transmembrane; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         le Jossec M., Cloix J.F., Pecquery R., Giudicelli Y., I "Differential sodium regulation between salt-sensitive resistant Sabra rats is not due to any mutation in the 2B-adrenoceptor gene.";
Am. J. Hypertens. 8:177-182(1995).
                                                                                                                                                                                                                                     DOMAIN
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EMBL; X74400; CAA52411.1; -.
PIR; A35642; A35642.
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MEDLINE=95275492; PubMed=7755946;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE 'INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH
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J.K., D'Angelo
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87:3102-3106(1990).
          BCA040FFF9A310EB CRC64;
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\ -> EP (IN REF.
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RESULT 3
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BINDING

Matches Query Match Best Local :

378;

61

Local

Similarity

83.3%;

Score 1981; DB 1; Length 453; pred. No. 9e-106; 4; Mismatches 45; Indels

4.

Gaps

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDILINE-92378586; PubMed=1354956;
Chruscinski A.J., Link R.E., Daunt D.A., Barsh G.S., Kobilka B.K.;
"Cloning and expression of the mouse homolog of the human alpha 2-c2

Biochem. Biophys. Res. Commun. 186:1280-1287(1992).

-!- FUNCTION: ALPHA-2 ADRENNERGIC RECEPTORS MEDILATE THE CATECHOLAMINE-
INDUCED INHIBITION OF ADENVLATE CYCLASE THROUGH THE ACTION OF G-
-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- SUBCELLULAR LOCATION: Integral membrane protein.
         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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PROSITE; P800237; GPROTEIN RECEP_F1 2; 1.
G-protein coupled receptor; Transmembrane; Multigene family;
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GO; GO:0004938; F:alpha2-adrenergic receptor
GO; GO:0001525; P:m3piogenesis; JMP.
GO; GO:000165; P:mAPKKK cascade; IMP.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1, 1.
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EMBL; L00979; AAA37131.1; ALT_INIT.
PIR; S28221; S28221
HSSP; P29274; 1MMH.
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STRAIN=DBA/2; TISSUE=Liver;
MEDLINE=93129622; PubMed=1336396;
Chen W.-M., Chang A.C., Shie B.J., Chang Y.
"Molecular cloning and characterization of adrenoceptor subtype gene.";
Bicchim. Biophys. Acta 1171:219-223(1992).

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Alpha-2B adrenergic ADRA2B.

Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Mammalla; Eutheria; Rodentia; NCBI\_TaxID=10090;

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Pfam; PF00001; GFCRRHODOPSN.

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HSSP; P29274; 1MMH.
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor)
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             requires a license agreement (Some email to license@isb-sib.ch).
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BELONGS TO
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151
297
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Chordata; Craniata; Vertebrata;
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O FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CYTOPLASMIC (P.
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EXTRACELLULAR
7 (POTENTIAL).
BY SIMILARITY.
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2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL)

3 (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL)
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4 (POTENTIA)
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                                                                                                                                     (POTENTIAL).
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15-JUL-1998
28-FEB-2003
                                                                                      entities
or send a
                                                                                                                                                                                                             "Endemic African "..."
"Endemic African "..."
Nature 388:61-64(1997)
Nature 388:61-64(1997)
Nature 388:61-64(1997)
                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE=97357151; PubMed=9214502;

Springer M.S., Cleven G.C., Madsen
Amrine H.M., Stanhope M.J.;

"Endemic African mammals shake the
PRINTS; PR00237; GPCKRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
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15-JUL-1998 (Rel. 36, Last sequence upd
28-FEB-2003 (Rel. 41, Last annotation u
Alpha-2B adrenergic receptor (Alpha-2B
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                                                   InterPro;
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SIMILARITY: BELONGS TO
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                                                                                      requires a license agreement (S
an email to license@isb-sib.ch).
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                                                522; CAA73122.2; ALT_SEQ.
IPR000276; GPCR_Rhodpsn.
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88.6%;
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OF G-PROTEIN COUPLED RECEPTORS
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3 adrenoceptor)
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Orycteropus.
                                                                                                                                                                                                                                                                                                                                                                                          (Fragment).
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E ACTION OF G
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coupled

Lipoprotein;

Palmitate.

receptor;

Transmembrane; Multigene family;

TRANSMEM DOMAIN

140 156 180 352 376 385 >385 >388 151 291

6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL) EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).

(POTENTIAL).

(POTENTIAL)

TRANSMEM DISULFID DOMAIN SITE

BY SIMILARITY,
ASP/GLU-RICH (ACIDIC)
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SIMILARITY)

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1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
2 (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).

1 26 37 63 73 96 118 118 141 157 181 157 181 353 377 386

Query Match Best Local S Matches 345

Similarity 87.1 45; Conservative

74.7%; 87.1%;

15;

Score 1775.5; Pred. No. 3.5e L5; Mismatches

5.5; DB 1; Length 3.5e-94; ches 27; Indels

388;

9,

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NON TER SEQUENCE

388 388 AA;

388 42429

MW;

1810DC767E838897 CRC64;

SITE SITE

167

167 163

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74 LLGYWYFRRTWCBVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTFRRIKCII
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PROSITE; PS00237; G_PROTEIN RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Y15945; CAA75898.2; -.
HSSP; P29274; LMMH.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam, PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMMEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way endified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stanhope M.J., Madsen O.J., Waddell V.G., Springer M.S.;
"Highly congruent molecular support for a of endemic African mammals.";
Mol. Phylogenet. Evol. 9:501-508(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
MEDLINE=98334573; PubMed=9667998;
MEDLINE=98334573; PubMed=9667998;
Cleven G.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Madsen O.J.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVISIONS
            121
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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             LTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGSFFAPCLIMILVYL
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LTVWLIAAVISLEELIYKGDQGPQERGREQCKLNQEAWYILASSIGSEEAECLINILVYL
                                                      AIAAAITFLILETIFGNALVILAVLTSRSLRAPQNLFLVSLAAADILVATLIIPESLANS
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                                                                                      AIAAVITELILETIEGNALVILAVLTSRSLRAPONLELVSLAAADILVATLIIPESLANE
                                                                                                                                                                                       389 AA;
                                                                                                                                            Conservative
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141
181
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                                                                                                                                                                                     389
42257 MW;
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36
62
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75
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140
156
180
363
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                                                                                                                                                    74.6%;
89.5%;
                                                                                                                                          11;
                                                                                                                                                                                                      IMPLICATED IN LIGAND BINDING (I
SIMILARITY).
IMPLICATED IN CATECHOL AGONIST
(BY SIMILARITY).
IMPLICATED IN CATECHOL AGONIST
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                   1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                              3 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

4 (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).
                                                                                                                                     Score 1775; DB 1;
Pred. No. 3.7e-94;
1; Mismatches 24;
                                                                                                                                                                                                                                                                              6 (POTENTIAL).
EXTRACELLULAR
BY SIMILARITY.
POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                992179431679B0FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
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                                                                                                                                                           Length
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                                                                                                                                                                                                                   AGONIST
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                                                                                                                                                                                                                 BINDING
                                                                                                                                   Gaps
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                                                                 133
                                           120
                                                                                       60
                                                                                                             73
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ADRA2B.

Equus Caballus (Horse).

Eukaryota; Metazoa; Choro
Mammalia; Eutheria; Peri

NCBI\_TaxID=9796;

Chordata; Craniata; Vertebrata; Perissodactyla; Equidae; Equus.

Euteleostomi; (Fragment).

Alpha-2B

999 (Rel. 38, Created)
001 (Rel. 40, Last sequence upo
001 (Rel. 40, Last annotation under the compared of the

update)

update) 3 adrenoceptor)

RESULT A2AB\_HO

A2AB HORSE 077721; 15-JUL-1999 16-OCT-2001 16-OCT-2001

STANDARD;

PRT;

389

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문 Ś 닭 Ş 밁 Ś 뭐 Ş 8 ઈ 밁 Ş 밁 Ś

353 373 293 313 240 253 181

LAVVIGVEVLCWEPEFESYSLGAICPKHCKVPHGLF LAVVIGVEVLCWEPFFFSYSLGAICPQRCKVPHGLF

408 388

TGEK-EGKTPEDPGTLTLPPSWPAFPNSGEGQKEGICGTSPEEEA-----

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RESULT 8
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                                                                                                                                                                                                                                                                     HSSP; P29274; 1MMH.
InterPro; IPRO00276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
Pfam; PF000237; GFCRHODOPSN.
PRINTS; PR00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
G-protein_coupled_receptor; Transmembrane; Multigene family;
                                                                                                                                  TRANSMEM
DOMAIN
TRANSMEM
                           TRANSMEM
DOMAIN
                                                                                           DOMAIN
TRANSMEM
                                                                                                                                                                                                                            NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE-97357151; PubMed-9214502;

Springer M.S., Cleven G.C., Madsen O.J., de Jong W.W., I
Amrine H.M., Stanhope M.J.;

"Endemic African mammals shake the phylogenetic tree.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Erinaceus europaeus (Western European hedgehog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Insectivora; Erinaceidae; Erinac
                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Y12521; CAA73121.1; -. HSSP; P29274; 1MMH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36,
15-JUL-1998 (Rel. 36,
16-OCT-2001 (Rel. 40,
Alpha-2B adrenergic re
                                                                                                                                                                                                                                              Phosphorylation;
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 388:61-64(1997).
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SUBCELLULAR
SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALAS-VASAREVNGHSKS
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         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1
BELONGS TO
      25
62
72
72
117
1140
1156
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355
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0, Last annotation update)
receptor (Alpha-2B adrenoceptor)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Integral membrane protein.
O FAMILY 1 OF G-PROTEIN COUPLED
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1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

3 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

4 (POTENTIAL).

5 (POTENTIAL).

5 (POTENTIAL).

5 (POTENTIAL).

6 (POTENTIAL).
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ceinae; Erinaceus.
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RESULT 9
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Best Local Similarity
                                                                                                                                                                                                            A2AB ELEMA
019014;
15-JUL-1998
15-JUL-1998
16-OCT-2001
                                               SEQUENCE FROM N.A.

MEDLINE-97357151; PubMed-9214502;

Springer M.S., Cleven G.C., Madsen O.J., de Jong W.W., lancine H.M., Stambope M.J.;

"Endemic African mammals shake the phylogenetic tree.";

"Endemic African mammals shake the phylogenetic tree.";

"Auture 388:61-64(1997).

"INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE
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This
                                                                                                                                                                                                   Alpha-2B adrenergic receptor
                  PROTEINS.
SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
SWISS-PROT
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                                                                                                                                                                                                                                                                                                          LAVVIGVEVLCWFPFFFFSYSLGAICPKHCKVPHGLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGSFFAPCLIMILVYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTPRRIKCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIAAVITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADILVATLIIPFSLANE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     391
391 AA;
                                                                                                                                                                                                        (Rel. 36, Created)
(Rel. 36, Last sequence up
(Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167
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                                                                                                                                                                                                                                                        STANDARD;
entry
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>391
151
294
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42919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.5%;
87.4%;
8
                   W: Integral membrane protein TO FAMILY 1 OF G-PROTEIN COL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
BY SIMILARITY.
ASP/GLU-RICH (ACIDIC).
IMPLICATED IN LIGAND BINDING (INTELLICATED IN CATECHOL AGONIST (BY SIMILARITY).
IMPLICATED IN CATECHOL AGONIST (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1771; DB 1;
Pred. No. 6.3e-94;
                                                                                                                                                                                                  (Alpha-2B
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3 adrenoceptor)
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PRINTS; PR00237; GFCRRHODDSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Transmembrane; Phosphorylation; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phosphorylation;
NON_TER 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no rest; use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@sisb-sib.ch).
                                                                                                                                                                                                                                                              14 AIAAAITELILETIEGNALVILAVLTSRSLRAPQNLELVSLAAADILVATLIIPESLANE
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         LAVVÍGVEVLCWEÞFFFSÝSLGAICÞQHCKVÞHGLF
                      LAVVIGVFVLCWEPFEFSYSLGAICPKHCKVPHGLF 408
                                             PÁVPAŠ PALAČŠ PELOOPKIS RVLATLRGOVILIGRGVIGTAGGOWKRRRAOLTREKRFTFV
                                                           OAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFTFV
                                                                                   PGEKÉR-ÉTPÉDPGTLTLÉPÉSMPVLPNSGQGQKEGVCGASP------EEÉEBECGS
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                                                                                                                           RIYLIAKRSNRRGPRAKGAPREGEPKOPHPLPAGPSALANSPTLASSLAVTGEANGHSEP
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INCLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).

IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                        Score 1748.5;
Pred. No. 1.2
                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.

ASP/GLU-RICH (ACIDIC).

IMPLICATED IN LIGAND BINDING
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7 (POTENTIAL)
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5 (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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2 (POTENTIA)
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          384
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                                                                                                                                                                                                                                                                                                              Length 384;
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386 AA;
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EMBL; Y12526; CAA73126.2; -. HSSP; P29274; IMMH.
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE=97357151; PubMed=9214502;
Springer M.S., Cleven G.C., Madsen
Amrine H.M., Stanhope M.J.;

"Endemic African mammals shake the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A2AB AMBHO
018935;
15-JUL-1998
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amblysomus hottentotus (Hottentot golden mole).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Insectivora; Chrysochloridae; An
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
ADRA2B.
                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             African mammals shake the phylogenetic tree.";
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PRINTS; PR00237; GPCRRHODOPSN. PROSITE; PS00237; G\_PROTEIN\_RE InterPro; IPR000276; GPCR\_Rhodpsn. Pfam; PF00001; 7tm\_1; 1. PS00237; G\_PROTEIN\_RECEP\_F1\_2; 1.
PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.
Coupled receptor; Transmembrane; Multigene family; Lipoprotein; 3 (POTENTIAL).
CYTOPLASMIC (P. 7 (POTENTIAL).
ASP/GLU-RICH (ACIDIC).
BY SIMILARITY
IMPLICATED IN LIGAND BINDING
SIMILARITY). IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
IMPLICATED IN CATECHOL AGONIST BINDING EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL) 4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL)

5 (POTENTIAL). 1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL) (BY SIMILARITY) CYTOPLASMIC Palmitate. (POTENTIAL) (POTENTIAL). (POTENTIAL). (BY

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                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=9833-3...
Stanhope M.J., Madsen O.J., Waddell v...,
Springer M.S.;
Springer M.S.;
"Highly congruent molecular support for a dive
"Highly congruent molecular support for a dive
f of endemic African mammals.";
Mol. Phylogenet. Evol. 9:501-508 (1998).
L. Mol. Phylogenet. Evol. 9:501-508 (1998).
C. -I- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS ME
C. -I- FUNCTION: INHIBITION OF ADENYLATE CYCLASE T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches 345
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_A2AB_BOV
_O77700;
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16-OCT-2001
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98334573; PubMed=9667998; MEDLINE=98334573; PubMed=9667998; Maddell V.G.,
                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstati the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entitles requires a license agreement (see http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                                                EMBL; Y15944; CAA75897.2;
HSSP; P29274; 1MMH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
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SIMILARITY: BELONGS TO
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PROSITE; PS00237; G PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Multigene family.

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Matches
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Best Local (
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PF10001; 7tm 1; 1.
PROSTITE; PS00237; GPCRENGDDPSN.
PROSTITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein_coupled_receptor; Transmembrane; Multigene family;
G-protein_coupled_ricoprotein; Palmitate.
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MEDLINE=97357151; PubMed=9214502;

Springer M.S., Cleven G.C., Madsen O.J., de Jong W.W., I
Amrine H.M., Stanhope M.J.;
"Endemic African mammals shake the phylogenetic tree.";
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-!- SIMILARITY: BELONGS TO
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194 RIYLIAKRSNRRGDRAKGGPGQGESKQPRPDHGGALASAKLPALAS-VASAREVNGHSKS
                                                134 LTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGSFFAPCLIMILVYL
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                                                                                       13
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                                                                                                                                        14 AIAAAITELILETIFGNALVILAVLTSRSLRAPQNLELVSLAAADILVATLIIPESLANE
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                                   LMVWLIAAVISLESLVYKGDQGPQPSGAPQCNLNQETWYILASSIGSFFAPCLIMILVYL
                                                                                            LLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTFRRIKGII
                                                                                LLGYWYFRRMWCKVYLALDVLFCTSSIVHLCAISLDRYWAVSRALBYNSKRTFRRIKCTI
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TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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Pred. No. 2
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16-OCT-2001
28-FEB-2003
                                                                                                                                                                                                         G-protein
NON_TER
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-!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CINDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE
                                                                                                                                                                                                                                                       InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
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                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.
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                                                                                                                                                                                                                                                                                           EMBL; Y15947; CAA75900.2; -. HSSP; P29274; 1MMH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Sirenia; Dugongidae; Dugong.
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor)
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                                                                                                                                                                                                                                PS00237;
PS50262;
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G_PROTEIN_RECEP_F1 2; 1.
receptor; Transmembrane; Multigene family.
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36
72
MW;
                                                                                                                                      2 (POTENTIAL).
EXTRACELLULAR
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                        EXTRACELLULAR (POTENTIAL)
ASP/GLU-RICH (ACIDIC).
BY SIMILARITY.
                                                              CYTOPLASMIC (POTENTIAL). 6 (POTENTIAL).
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RESULT 14
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the Euro
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HSSP; P29274; 1MMH.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; GPCRRHODOPSN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Procavia capensis habessinica (Abyssinian hyrax).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Mammalia; Eutheria; Hyracoidea; Procaviidae; Procavia.
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MEDLINE=97357151; PubMed=9214502;
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                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation. Buropean Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no wifified and this statement is not removed. Usage by and for commercial field and this statement is not removed.
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                                                                                                                                                                     s requires a license agreement (See http://www.isb-sib.
an email to license@isb-sib.ch).
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RESULT 15 A2AB\_MACPR

A2AB MACPR

STANDARD;

387 AA

CARREDAN

Alpha-28 ADRA28.

adrenergic

Macroscelides proboscideus (Short-eared elephant shrew) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut Mammalia; Eutheria; Macroscelidea; Macroscelididae; Mac

Euteleostomi;

019025; 15-JUL-1998 16-OCT-2001 16-OCT-2001

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          LAVVIGVFVLCWFPFFFSYSLGAICPKHCKVPHGLF
                                              QAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAQLTRBKRFTFV
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Springer M.S., Cleven G.C., Madsen O., de Jong W.W., Waddell V.G.,
Amrine H.M., Stanhope M.J.;

Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
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MEDLINE=97357151; PubMed=9214502;
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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  61
                                       74
                                                                                                                                                                               Similarity
                    LLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTPRRIKCII 133
                                                                          AIAAAITELILETIFGNALVILAVLTSRSLRAPQNLELVSLAAADILVATLIIPESLANE 73
  LLGYWYFRHTWCXVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTPRRIKCII
                                                                                                                                                                                                                                       387
387 AA;
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26
27
37
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37
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118
118
                                                                                                                                                             Conservative
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62
72
                                                                                                                                                                             71.3%;
                                                                                                                                                                                                                                         42587 MW;
                                                                                                                                                       ; Score 1696; DB 1;
; Pred. No. 1.1e-89;
13; Mismatches 37;
                                                                                                                                                                                                                                                                             IMPLICATED IN LIGAND BINDING (BY SIMILARITY).

IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).

IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                   ASP/GLU-RICH (ACIDIC).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC
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CYTOPLASMIC (
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                                                                                                                                                           37;
                                                                                                                                                                                                                                           CRC64;
                                                                                                                                                                                                Length 387;
                                                                                                                                                             Indels
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351
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                                                                                                                                                                                                              LTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQBAWYILASSIGSFFAPCLIMILVYL 193
               VLAVVIGVFVLCWFPFFFSYSLGAICPKHCKVPHGLF
                                                                                                       PTGER---ETPEDLVSPASPPSWPAIPNSGQGRKEGVCGTSPEEEA-----EEEEECG
                                                                                                                     STGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEEEEEEEEEEEEEE 311
                                                                                                                                                            RIYLIAKRSSSRKKPRAKGXPREGESKQPQLRPVGTSVSARPPALTSPLAVTGEANGHSK
                                                                                                                                                                          RIYLIAKR-SNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALAS-VASAREVNGHSK
                                                  PEAVPASPALACSPSLQPPQGSRVLATLRGQVLLGRGVGTARGQWWRRRAQLTREKRFTF
                                                                     PQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFTF
VLAVVIGVEVLCWFPFFFSYSLGAICPQHCKVPHGLF
 387
                          408
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Search completed: February 6, Job time : 11.0334 secs 2004, 18:18:03

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Run on:
   SPTREMBL 23:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fung1:*
4: sp_hunan:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
9: sp_bhage:*
10: sp_plant:*
11: sp_virus:*
12: sp_virus:*
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Gapop 10.0 , Gapext 0.5
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2378
1 MDHQDPYSVQATAAIAAAIT.....QDFRRAFRRILCRPWTQTAW 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pebruary 6, 2004, 18:11:25 ; Search time 33.1104 Seconds (without alignments) 3507.169 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
sp_lant:*
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sp_unclassified:*
sp_rvirus:*
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sp_barcheap:*
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sp_phage:*
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sp_mammal:*
sp_mhc:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

16	15	14	13	12	11	10	9	8	7	o,	S	4	ω	2	1	Result
1814	1824.5	1828	1833	1841	1842	1843	1844	1855	1855	1856	1885	1945	1950	1999	2139.5	Score
76.3	76.7	76.9	77.1	77.4	77.5	77.5	77.5	78.0	78.0	78.0	79.3	81.8	82.0	84.1	90.0	Query Match Length
399	390	399	389	387	391	395	395	399	393	397	401	448	448	453	451	Length
Q	σ	σ	σ	σ	σ	11	თ	9	σ	11	σ	11	片	片	9	DB
Q8MIE3	Q9GL19	Q8MK51	Q9GL07	Q9GL17	Q9GL06	QBK1U9	Q9GL12	Q8MID0	Q9GL11	QBK1W6	Q8MK45	Q925K6	Q925K7	Q925E4	<b>ОВН</b> УУВ	ID
Q8mie3 lepus craws	Q9gl19 cynocephalu	Q8mk51 lama guanic	Q9gl07 phoca vitul	Q9gl17 felis silve	Q9gl06 sus scrofa	Q8klu9 erethizon d	Q9gl12 manis sp. a	Q8mid0 manis tetra	Q9glll nycticebus	Q8klw6 castor cana	Q8mk45 tapirus ter	Q925k6 mus musculu	Q925k7 mus musculu	Q925e4 rattus norv	Q8hyy8 tupaia bela	Description

45 1760.5		43 1769.5		41 1772		39 1774.5	38 1776	37 1776	36 1776.5	35 1778.5	34 1779	33 1782	۳,	31 1786	30 1787		28 1790.5	27 1791	26 1792.5	25 1795		23 1798.5	22 1806	21 1806.5		19 1807.5	18 1808	17 1811
74.0	74.4	74.4	74.5	74.5	74.5	74.6	74.7	74	74.7	74	74.8	74	-			_	•		•	75	_	75	75	76.0	76	76.0		76.2
400	391	392	392	391	391	394	395	389	392	406	391	389	388	395	393	393	388	389	388	389	393	390	395	392	393	398	395	389
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Q8hxm4 galemys pyr	Q8mie5 hylomys sui	Q95n90 tadarida br	Q8k4y3 sciurus vul	Q8k1r1 massoutiera	Q8hy23 physeter ca	Q8sqa1 desmodus ro	Q8klu7 myoxus glis	Q8k1w8 bathyergus	Q9gl35 balaenopter	Q8kln6 thomomys ta	Q8sqa0 emballonura	Q95n94 hipposidero	Q9gl18 diceros bic	Q8sq94 noctilio al	Q9jjw2 cavia porce	Q8k1p2 trichys fas	Q8sq91 nycteris th	Q8cg78 chinchilla	Q8sq93 nycteris gr		Q9gl16 hippopotamu	Q95n89 taphozous s	Q8k3r6 anomalurus	Q8klu3 marmota mon	Q8miel lama guanic	Q8sq92 natalus str		Q9gkz5 tupaia tana

## ALIGNMENTS

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181 FFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALA-S 239	121 NSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGS 180	121 NSKTTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGS 180	61 VATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEY 120	61 VATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEY 120	1 MVHQEPYSVQATAAIAAVITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADIL 60	1 MDHQDPYSVQATAAIAAAITFLILFTIFGNALVILAVLTSRSLRABQNLFLVSLAAADIL 60	Matches 411; Conservative 8; Mismatches 31; Indels 1; Gaps 1;	Match 90.0%;	SEQUENCE 451 AA; 50356 MW; 3172403011F3BC60 CRC64;	0333: AAN72436.1:	Submitted (SEP-2002) to the EMBI/GenBank/DDBJ databases.	upregulation in the paraventricular nucleus ettess. Persustent	adrenocentors under chronic stress:	Tourish B Bluesse			ae; Tupaia.	Eukarvota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:	Alpha-28 adrenceptor. Three belanceri (Northern tree chrew)	. 23, Last	(TrEMBLrel. 23,	QBHYYB; 01-MAR-2003 (TrEMBLrel. 23, Created)	Q8HYY8 PRELIMINARY; PRT; 451 AA.	Y8

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Query Match
Best Local S
Matches 380
                                                                                                                                                                                                                                                                                                                                                    -1- SUBJECTALULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SI -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED R EMBL; AF36699; AAK53388.1; -...

**Interpro;** IPRO00276; GPCR. Rhodpsn.**

**Pfam; PF00001; 7tm 1; 1.*

**Pfam; PF00001; 7tm 1; 1.*

**PRINTS; PR00237; GPCRHODDPSN.**

**PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.*

**R PROSITE; PS00237; GPROTEIN RECEP F1 2; 1.*

**R PROSITE; PS00262; GPROTEIN RECEP F1 2; 1.*

**G-protein coupled receptor; Receptor; Transmembrane.**

**G-protein coupled receptor; Receptor; CRASSCESSEACBS11 CRC64;

**SEQUENCE 453 AA; 50369 MW; CBASSCE23EACBS11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene promoter.";
gene promoter.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
-!- SUBCELLULAR HOLONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Sprague-Dawley,
Schaak S., Cussac D., Paris H.,
"Cloning and characterization of the rat alpha2B-adrenergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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[1]
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 23,
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                       LSŚVGĖANGHPKPPRĖKĖBGĖTPEDPBARALPPTWSALPRŠGOOKKGTSGATAĖ---ĖG
                                         VASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGGGKEGVCGASPEDEAEE
                                                                                            FFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALAS-
                                                                                                                                  NSKRTPHRÍKCIÍLTVMLÍAAVÍSLPPLÍYKGDÓRÞEÞRGLÞÓCELNQEAWYÍLASSIGS
                                                                                                                                                  Similarity
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                                                                            PPAPCLÍMILVÝLRÍÝVÍAKRÍSHCRÍGLGÁKRÍSSGEGEŠKKÞOÞVAGGVPTŠÁKVÞTLVSÞ
                                                                                                                                                                                                         VATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEEEEEEEECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LATAGEANGHSKPPCNREDGETPEDPGTRVLPPSWAALASSCCCOKEGVREASAEEEEEE
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Pred. No. 4.9e-152;
5; Mismatches 42;
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Last annotation updat
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Sciurognathi; Muridae; Murinae; Rattus
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Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00037; GFCRRHODDPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1 1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1 2; 1.
G-protein_coupled_receptor; Receptor; Transmembrane.
SEQUENCE 448 AA; 50018 MW; 1B5ED9456C0B2B73 CRC6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bringer W.A., Thompson J., Conroy O., Xu Y., Yang F., Car Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.! "High-Throughput Sequence Identification of Gene Coding V. within Alcohol-Related QTLS.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SEMEL; AP332049; AAX56078.1; -.
EMBL; AP332049; AAX56078.1; -.
MGD; MGI:87935; Adra2bb.
MGD; MGI:87935; Adra2bb.
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Q925K7;
Q1-DEC-2001
01-DEC-2001
01-MAR-2003
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-MAR-2003 (TrEMBLrel. 23, Last annotation
Addrenergic receptor alpha 2B.
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                                                             FFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGESKQPRDDHGGALASAKLPALAS-
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Pred. No. 4.1e-148;
2; Mismatches 49;
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MGD; MGI:87935; Adra2b.

InterPro; IPR000276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm 1; 1.

PROSITE; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN RECEP_F1_2; 1.

PROSITE; PS50262; G_PROTEIN RECEP_F1_2; 1.

G-protein coupled receptor; Receptor; Transmembrane.

SEQUENCE 448 AA; 49998 MW; B37E5E21B0EC4625 CRC6
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-DEC-2001 (TYEMBLrel. 19, Last sequence update)
01-MAR-2003 (TYEMBLrel. 23, Last annotation update)
Adrenergic receptor alpha 2B.
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Beeson M., Gordon L., Bennett B., Johnson
"High-Throughput Sequence Identification o
within Alcohol-Related QTLB.";
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Best Local S
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Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINS=21608557; PubMed=11743200;
MUTPhy W.J., Bizirik E., O'Brien S.J., Madsen
Douady C.J., Teeling E., Ryder O.A., Stanhope
Springer M.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tapirus terrestris (Lowland tapir) (Brazilian tapir).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Perissodactyla; Tapiridae; Tapirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence up
01-MAR-2003 (TrEMBLrel. 23, Last annotation
Alpha 2B adrenergic receptor (Fragment).
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01-OCT-2002
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Pred. No. 5.8e-143;
2; Mismatches 20;
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Q9GL11 PRELIMINARY;
Q9GL11,
Q1-MAR-2001 (TrEMBLrel. 16, C
01-MAR-2001 (TrEMBLrel. 22, L
Alpha adrenergic receptor 2B
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Best Local S
Matches 359
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Huchon D., Madsen O., Sibbald M.J.J.B., Ament Catzefils F., de Jong W.W., Douzery E.J.P.;

"Rodent phylogeny and a timescale for the every dence from an extensive taxon sampling us;

Mol. Biol. Evol. 0:0-0(2002);

EMBL; AJ427260; CAD20298.1; -

InterPro; 1PR00276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm_1; 1.

R PRINTS; PR00237; GPCRHODDPSN.

R PROSITE; PS00237; GPROTEIN_RECEP_F1_2; 1.

R PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
Alpha 2B adrenergic receptor
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Q8K1W6;
Q1-QCT-2002
Q1-QCT-2002
Q1-MAR-2003
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=51338;
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397
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     2B
       Created)

Last sequence update)

Last annotation update
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Sciurognathi, Castoridae,
                                                                                  393
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annotation updat
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RESULT 8
Q8MID
ID Q8MI
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OC Euka
OC Mamm
OX NCBI
RN [1]
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Q8MIDO;
01-OCT-2002 (TIEMBLIEL 2
01-OCT-2002 (TIEMBLIEL 2
01-MAR-2003 (TIEMBLIEL 2
01-MAR-2003 (TIEMBLIEL 2
Alpha 2B adrenergic recept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 361
 Manis tetradactyla (Long-tailed pangolin)
Eukaryota; Metazoa; Chordata; Craniata; V.
Mammalia; Eutheria; Pholidota; Manidae; M.
NCBI_TaxID=73815;
[1]
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PROSITE; P800237; G PROTEIN RECEP F1 1; 1.

PROSITE; P850262; G PROTEIN_RECEP F1 2; 1.

G-protein coupled receptor; Receptor, Transmembrane.

NON_TER 1 1
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-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; AJ251186; CAC16695.1; -
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MEDLINE=21082081; PubMed=11214318;
Madsen O., Scally M., Douady C., Kao
Amrine H., Stanhope M., de Jong W., S
"Parallel adaptive radiations in two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 409:610-614(2001).
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Mycticebus coucang (Slow loris).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Strepsirhini, Loridae; Nycticebus.
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                                                                                                                                                                                                                                QAVPVSPASACSPELQOPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRPTFV 372
                                                                                                                                                                                                                                                                    PGEKEEGÉTLEDVGSŘPĹPPGWAALSNSGOGOKEGVCGÁSPÉEEA--
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                                                                                                                         PRELIMINARY;
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393 AA;
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                                                            Lrel. 22, (Lrel. 22, I
Lrel. 23, I
creceptor
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4; 42990 MW;
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91.2%; Pred. No. 1.4e
Live 11; Mismatches
                                                        , Last sequence up
, Last annotation
or (Fragment)
                                                                                                Created)
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, Springer M.;
wo major clade
          Vertebrata;
Manis.
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                  Euteleostomi;
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Best Local S
Matches 362
mammals.";

Nature 409-610-614(2001).

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
-i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COU
EMBL; AJ251185; CAC16694.1; -.

ThterPro; IPR000276; GPCR_Rhodpsn.
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Q9GL12;
Q1-MAR-2001
01-MAR-2001
01-OCT-2002
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Madden O., Willemsen D., Ursing B.M., Arnason U., de Jong W.

"Molecular evolution of the alpha 2B adrenergic receptor.";

Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ505820; CAD44321.1; -.

InterPro; IPR000276; GPCR_Rhodpsn.

Pfam; PF00001; Ttm 1; 1.

PR.NTS; PR00237; GPCRRHODDPSN.

PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=21082081; PubMed=11214318;
MEDdine=21082081; PubMed=11214318;
Madden O., Scally M., Douady C., Kao
Amrine H., Stanhope M., de Jong W., S
"Parallel adaptive radiations in two
                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa,
Mammalia, Eutheria,
NCBI_TaxID=49127;
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                                                                                                                                                                                                                                                                                                                                                                                             R-2001 (TrEMBLrel. 16, Created)
R-2001 (TrEMBLrel. 16, Last sequence update)
T-2002 (TrEMBLrel. 22, Last annotation update)
adrenergic receptor 2B (Fragment).
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Pholidota;
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; Manidae;
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                                                                                                                                                             Kao D., DeBry R.
W., Springer M.;
two major clades
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                                                                              G-PROTEIN COUPLED
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  InterProj IPR000276; GPCR_Rhodpsn.

Pfam; pF00001; 7tm_1; 1.

PRINTS; PR00237; GPCRRHODDPSN.

PROSITE; pS00237; GPROTEIN_RECEP_F1_1; 1.

PROSITE; pS50262; G_PROTEIN_RECEP_F1_2; 1.

Receptor.

NON_TER 395 395

SEQUENCE 395 AA; 43157 MW; 9E46A1E10EE
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PRINTS; PR00237; GPCRTODOPSN.

PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.

PROSITE; PS50262; GPROTEIN RECEP F1 2; 1.

PROSITE; PS50262; GPROTEIN RECEPT F1 2; 1.

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PROSITE: PS60262; GPROTEIN RECEPT F1 1; 1.

PROSITE: PS
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Mol. Biol. Evol. 0:0-0(2002).
EMBL; AJ427270; CAD20308.1; -
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Huchon D., Madsen O.,
Catzeflis F., de Jong
"Rodent phylogeny and
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Hystricognathi; Ereth
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-! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
INterPro; IPR000276; GPCR.Rhodpsn.
Pfam; PF00001; 7tm 1, 1.
PRINTS; PR00237; GFCRRHODDPSN.
PROSITE; PS00237; GPCRRHODDPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; GPROTEIN_RECEP_F1_2; 1.
G-PROTEIN_RECEP_F1_2; 1.
G-PROTEIN_RECEP_F1_2; 1.
G-PROTEIN_RECEP_F1_2; 1.
G-PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDILINE=21082081; PubMed=11214318;

Madsen O., Scally M., Douady C., Kao D., DeBry R., Adkins
Ammine H., Stanhope M., de Jong W., Springer M.;

"Parallel adaptive radiations in two major clades of place
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Best Local Similarity
Matches 356; Conserv
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-OCT-2002 (TrEMBLrel. 22, Last annotation
alpha adrenergic receptor 2B (Fragment).
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Mammalia; Eutheria;
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391 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFTFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIYLIAKRSHRRGÞRÁKGGÞGEGESNOSRÞVÞGGÁÞÁSÁKVÞÞLÁSÞLSSÁGEANGHÞKÞ
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                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATĀĀVĪTĒLĪLĒTĪ ĒGNĀLVĪLĀVLTSRŠLRĀÞONLĒLVSLĀĀĀDĪLVĀTLĪ ĪPĒSLĀNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                         391
; 42846 MW;
                                                                                                                      77.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
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                                                                                               12;
                                                                                      Score 1842; DB
Pred. No. 1.6e-
12; Mismatches
                                                                                                                                                                  76A4F0FA3EC74F16 CRC64;
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Pred. No. 1.3e-139;
.4; Mismatches 24;
                                                                                    .6e-139;
les 22;
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                                                                                                                      Length 391;
                                                                                    Indels
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Sus.
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Q9GL17
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SEQUENCE
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Q9GL17;
Q9GL17;
Q9GL17;
Q9GL17;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-CCT-2002 (TrEMBLrel. 22, Last annotation update)
Q1-CCT-2002 (TremBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                               InterPro; IPR000276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G PROTEIN_RECEP_F1 1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1 2; 1.

G-protein coupled receptor; Receptor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 409:610-614 (2001).

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SELECTION OF FAMILY 1 OF G-PROTEIN COUPLED EMBL; AJ251174; CAC16689.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLING=21082081; PubMed=11214318;

Madsen O., Scally M., Douady C., Kao D., DeBry R.,

Amrine H., Stanhope M., de Jong W., Springer M.;

"Parallel adaptive radiations in two major clades

menmands ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
                                                                                                  14 AIAAAITELILETIFGNALVILAVLTSRSLRAPQNLELVSLAAADILVATLIIPESLANB
                      61
                                                             74
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ilgywyfrkitwcevylaldvlfctssivhlcaisidrywavsraleyns
                  Similarity
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                                                                         ATAAVITĖLILĖTIĖGNALVILAVLTSRSLRAPONLĖLVSLAAADILVATLIIPESLANE
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                                                                                                                                                                                                                                                                    387
387 AA;
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42546 MW;
                                                                                                                                                                    77.4%; Score 1841; DB 6;
89.9%; Pred. No. 1.9e-139;
Live 12; Mismatches 20;
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Felis.
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Matches 356
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Q9GL07;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEAM; PF00001; 7tm 1; 1.

PRINTS; PR00237; GFCREHODOPSN.

PROSITE; PS00237; G-PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Receptor; Transmembrane
NON_TER 1 1

NON_TER 389 389

SEQUENCE 389 AA; 42278 MW; E42F177873FE47FF CRC4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NATURE 409:510-614 (2001).
-:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; AJ251176; CAC16696.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21082081; PubMed=11214318; Madsen O., Scally M., Douady C., Kao Amrine H., Stanhope M., de Jong W., S "Parallel adaptive radiations in two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phoca vitulina (Harbor seal).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Phoca.
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Pfam; PF00001; 7tm 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mammale.";
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                                                                                                                                            RIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALASVASAREVNGHSKST
                                                                           LTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGSFFAPCLIMILVYL
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                                                                                                                                                                                                                                                                               ATAAAITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADILVATLIIPFSLANE
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
ergic receptor 2B (Fragment).
                                                                                                                                                                                                                                                                                                                                                     Conservative
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90.1%;
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D7 Q1-Q0
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updatalpha 2B adrenergic receptor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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EMBL; AJ315941; CAC87005.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
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Murphy W.J., Eizirik E., O'Brien S.J.,
Douady C.J. Teeling E., Ryder O.A., S
Springer M.S.;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
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399 AA;
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26.8 330 15 26.5 29 23 6.5 29 24 5.8 457 22 5.8 458 25 5.8 461 22 5.8 330 17 5.6 330 17 5.6 330 17 5.6 450 22 5.6 450 22 5.1 24 19 5.1 29 17	G-protein	AAR48698	15	330	4.7	21	7
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26.8 330 15 6.5 29 23 6.5 29 24 5.8 457 22 5.8 458 22 5.8 461 22 5.8 461 22 5.6 330 17 5.6 330 17 5.6 450 22 5.6 450 22	Peptide effecting	AAW39955	19	24	5.1	23	_
26.8 330 15 6.5 29 23 6.5 29 24 5.8 457 15 5.8 461 22 5.8 461 22 5.6 330 17 5.6 330 17 5.6 450 22	Human alpha 2a-adr	ABP81779	24	450	5.6	25	٠
26.8 330 15 26.5 29 23 6.5 29 24 6.5 29 24 5.8 457 22 5.8 458 25 5.8 461 22 5.8 461 22 5.6 330 15 5.6 330 17 5.6 330 22	Human alpha-2AAR v	AAM52123	22	450	5.6	25	•
26.8 330 15 26.5 29 23 6.5 29 24 5.8 457 25 5.8 458 15 5.8 461 22 5.8 461 22 5.8 330 17	Human alpha-2AAR	AAM52122	22	450	5.6	25	_
26.8 330 15 6.5 29 23 6.5 29 23 5.8 457 15 5.8 461 22 5.6 461 22 5.6 330 15	G-protein coupled	AAW02672	17	330	5.6	25	_
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26.8 330 15 26.8 330 15 6.5 29 23 6.5 29 24 5.8 457 22 5.8 458 15 5.8 461 22	Human	ABP81781	24	461	5.8	26	~
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26.8 330 15 26.8 330 17 6.5 29 23 6.5 29 24 5.8 457 22	Human derived adre	AAR54834 ·	15	458	5.8	26	٠.
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26.8 330 15 . 26.8 330 17 . 6.5 29 23 .	Human alpha	ABP53986	24	29	6.5	29	_
26.8 330 15 . 26.8 330 17 .	G-protein	ABU67205	23	29	6.5	29	٠٠
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human alpha-2BAR third intracellular loop variant.
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Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a

Claim 20;

relates to

147-149; 163pp; English.

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CC (b) detecting a polymorphic site comprissing nucleotide positions 901-909 CC or a site comprising (A) (9990999900 or (B) (19909090900 at 1990) of (IIV) CC alpha2B, alpha2A or alpha2C receptor yene and further used to determine CC associated with alpha2B, alpha2B, alpha2B, alpha2B, alpha2B, alpha2B, alpha2B, alpha2B, alpha2B, alpha2B, alpha2B, alpha2B, alpha2B, alpha2B, alpha2B, alpha2B, alpha2B, alpha2B, alpha2B, alpha2B, or alpha2, comprising detecting a cC disease, central nervous system disease and combinations of these. In CC disease, central nervous system disease and combinations of these. In CC disease, the technique may be used to predict an individual's response combinations of these, or an alpha2A, or alpha2C agonist (e.g. epinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and CC rauwolscine, idazoxan, tolazoline, phantolamine and combinations of these) by detecting the polymorphic site and correlating the site to a cyclase, MAP kinase activity, phosphorylation or inositol phosphate che human alpha-2BAR variant protein, the sequence is deleted for the amino acid polymorphic site at residues 301-303 (EEE) of the wildtype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor gene (I)-(III) by detecting a polymorphic site, comprising; (a) obtaining a sample having a polymorphic site, comprising; alpha2A or alpha2C or fragment or complement of; and (b) detecting a polymorphic site or alpha-2B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease associated with the corresponding receptor comprises
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                                                                                                                                                                                                                                                               The present sequence is human alpha2B-adrenoceptor (alpha2B-AR) variant CC 298-309) of 12 9lutamates, in an acidic stretch of 18 amino acids canino CC acids 294-311, located in the third intracellular loop of the receptor CC polypeptide. The variant is obtained by deletion of three glutamates from CC chromosome 2. Alpha2-AR mediate many of the physiological effects of the CC catecholamines, norepinephrine and epinephrine. An antagonist of CC alpha2B-adrenoceptor is useful for treating a manmal suffering from CC vascular contraction of coronary arteries and a disease involving CC vascular contraction of coronary arteries which is clinically expressed CC clinically expressed as Prinzmetal's variant form or acute myocardial expressed CC clinically expressed as Prinzmetal's variant form or acute myocardial expressed CC infarction (AMI). Alpha2B-AR gene is used in gene therapy.
                                                                                                                                                                                        Best Local Similarity Matches 447; Conserv
                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of coronar
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121 NSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGS
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                                  vátlií prslánellgymy frrtincevy laldy lectssí vhlca i sldrymavskaley
                                                   MDHÓDÉÝSVÓATAÁIÁAÁÍTELÍLETÍEGNALVÍLÁVLTSRSLRÁÞONLELVSLÁAÁDÍL
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/note= "Glutamic acid repeat"
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Best Local Similarity
                                                    The invention relates to a method for detecting a risk of hypertension by determining the pattern of alleles encoding a variant alpha-2B-adrenoceptor (AR) protein. The methods and compositions of the invention are useful for detecting risks and targeting treatment for hypertension. The kit is also useful for selecting for clinical drug trials testing the antihypertensive effect of compounds. The present sequence is human alpha-2B-adrenoceptor variant.
                                 Sequence
                                                                                                                                                 Disclosure; Page 26-27; 35pp; English.
                                                                                                                                                                        Detecting a risk of hypertension and targeting treatment
by determining the pattern of alleles encoding a variant
alpha-2-adrenoceptor -
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
Synthetic.
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 17-APR-2000; 2000US-0551744
                      17-APR-2001; 2001WO-US12575
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                                                                                                                                                                                                               Region
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/label= polymorphic_site
/note= "Polymorphic site &
(AAMS22118)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC receptor gene (I)-(III) by detecting an alpha-2B, 2A, or 2C adrenergic CC (a) obtaining a sample having a polymorphic site, comprising; CC (a) obtaining a sample having a polymorphic site, comprising; CC (b) detecting a polymorphic site comprising uncleotide positions 901-909 (CC (b) detecting a polymorphic site comprising uncleotide positions 901-909 (CC or a site comprising cytosine or guanine at position 753 of (IIV) (CC positions 961-972 of (III). The method may be used for genotyping an elpha2B, alpha2A or alpha2C receptor gene and further used to determine CC associated with alpha2h are receptor gene and further used to determine CC disease, central nervous system disease selected from cardiovascular CC disease, central nervous system disease and combinations of these. In CC on alpha2B, alpha2A, or alpha2c agonist (e.g. epinephrine, clonidine, oxymetazoline, predict an individual's response CC or an alpha2B, alpha2A, or alpha2c agonist (e.g. epinephrine, comprising the end of these or alpha2c agonist (e.g. epinephrine, comprising the polymorphic site and correlating the site to a cc raiwolscine, idazoxan, tolazoline, phentolamine and combinations of these) by detecting the polymorphic site and correlating the site to a cc cyclase, MAP kinase activity, phosphorylation or inositol phosphate (complymorphic site and correlating the site to a cc cyclase, MAP kinase activity, phosphorylation or inositol phosphate CC uniman alpha-2Bap protein, the sequence is that of the third intracellular loop of colorant protein (AAMS2118).
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Best Local (
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                                                          241 ASAREVNGHSKSTGEKBEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDBAEBE
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60 60 Matches Query Match Best Local

306;

Conservative

Similarity

68.5%; 100.0%;

Score 306; DB 22; I Pred. No. 1.6e-271; 0; Mismatches 0;

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                 The present sequence is human alpha2B-adrenoceptor (alpha2B-AR) protein. Alpha2B-AR has a glutamic acid repeat element (amino acids 298-309) of 294-311), located in the third intracellular loop of the receptor mediate many of the physiological effects of the catecholamines. Princephrine and epinephrine and epinephrine and antagonist of alpha2B-arroceptor is coronary arteries which is clinically expressed as coronary heat disease involving vascular contraction of coronary arteries which is clinically expressed as coronary heat disease involving vascular contraction of coronary arteries which is clinically expressed as coronary heat disease Prinzmetal's variant form or acute myocardial infarction (AMI).
     Sequence
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Scheinin M,
                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 29-31; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of coronar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
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DB; AAD04762.
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Heinonen P, A...
Salonen JT,
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(T, Tuomainen T,
, Valkonen V;
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<sup>[</sup>, Lakka TA,
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                                                                                                         The invention relates to a method for detecting a risk of hypertension by determining the pattern of alleles encoding a variant alpha-2B-adrenoceptor (AR) protein. The methods and compositions of the invention are useful for detecting risks and targeting treatment for hypertension. The kit is also useful for selecting for clinical drug trials testing the antihypertensive effect of compounds. The present sequence is human alpha-2B-adrenoceptor protein.
                                                                                     Sequence
                                                                                                                                                                                                Disclosure; Page 30-31; 35pp; English.
                                                                                                                                                                                                                     alpha-2-adrenoceptor
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                                                                                                                                                                                                                                                            New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's diseas.
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The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (I) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity

Disclosure;

Fig 1; 523pp; English.

or autoimmune diseases

disease,

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CC or avidity for a particular GPCR. (1) can be used as GPCR modulators and CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting CC antibodies. The peptides and antibodies are also useful for detecting the CC presence or absence of corresponding GPCRs. The antigenic peptides for CC GPCRs and antibodies are useful for diagnosing and designing drugs for creating immune-related diseases, growth-related diseases, cell CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, CC diseases, allergies, Crohn's diseases, disease, cell costeoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute costeoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute disease, parkinson's disease, disease, disease, graft versus host canxiety, depression, schizophrenia, dementia, mental retardation, memory hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode cc GPCR proteins given in AbB981675 to ABB92018, which are used in the
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Best Local Similarity
Matches 306; Conserv
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100.0%; Pred. No. 1.6e-271;
tive 0; Mismatches 0;
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Matches 179; Conserv
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30-MAY-1991;
22-OCT-1992;
Assay for alpha-2b adrenergic receptor ligands -
                                                               WPI; 1997-107576/10.
N-PSDB; AAT59499.
                                                                                                                                          Hartig PR,
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                                                                                                                                                                                            (SYNA-) SYNAPTIC PHARM CORP
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06-MAY-1997
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N-PSDB; AAQ14151.
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                                                                                                                                       Weinshank
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Best Local
Proteins AAR48685-R48758 represent a range of G-protein coupled receptor proteins selected from cAMP, adenosine, muscarinic acetylcholine, adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G-protein coupled receptor; ligand binding assay; transmembrane domain; psychotic disorder; schizophrenia; dopamine; cAMP; adenosine; thrombin; muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human alpha-2B adrenergic receptor (AAW11804) is a member of the rhodopsin-like signal transducer family. Its amino acid sequence was deduced from a genomic DNA clone (AAR59499) obtd. from a human spleen DNA library. Vectors have been adapted to allow prodn. of alpha-2B adrenoceptor in bacterial, yeast or mammalian cells; transfected Ltk- cells, designated L-NGC-alpha-2B, are deposited as ATCC CRL 10275. Membranes of transfected mammalian cells can used in novel methods to identify drugs which specifically interact with, and bind to, the alpha-2B adrenergic receptor. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                       Disclosure;
                                                                                                                                                                           Polypeptides of G-coupled receptor proteins (GPRs) - useful binding GPR ligands or modulating GPR binding
                                                                                                                                                                                                                                                                                                                               Murphy
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                                                                                                                 72-73; 160pp;
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RESULT 11
AAW02671
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Best Local
                                                                                                                                                                    New dopamine receptor peptide - useful as antipsychotic agent, for treating schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                     G-protein coupled receptor; ligand binding assay; transmembrane domain; schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin; muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin; odorant; cytomegalovirus; serotonergic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of polypeptide fragments). The polypeptide fragments can be used in compositions for treating subjects suffering from a pathology related to a GPR abnormality e.g. a psychotic disorder such as schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         odorant, cytomegaloviral and other G-protein coupled receptors. The receptor proteins were used to design polypeptides, pref. based on the transmembrane domains, for use in G-protein coupled receptor ligand binding assays. The polypeptide fragments retain biological activity such as binding a GPR ligand or modulating GPR ligand binding to a GPR (see AR48759-R48758, ARR50569-R50807 and AR89189-R89195 for examples
                                                                                                                                                                                                            WPI; 1996-208785/21.
                                                                                                                                                                                                                                                                                        09-SEP-1993;
10-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G-protein coupled human alpha-2 C2 adrenergic receptor
                                                                                                                                                                                                                                                                                                                               09-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                           16-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                   US5508384-A
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW02671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW02671 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                               (UYNY ) UNIV NEW YORK STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
12-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAADILVATLIIPPSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRALEYNSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRALEYNSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             330 AA;
                                                                                                                                                                                                                                      Schuster DI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (updated)
(first entry)
                                                                                                                                                                                                                                                                                         93US-0118270.
92US-0943236.
                                                                                                                                                                                                                                                                                                                               93US-0118270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide; 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 120; DB 15;
Pred. No. 2.7e-101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₿
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 330;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163
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Proteins AAW02657-W02720 represent a range of G-protein coupled receptor (GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine, adarenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin, odorant, cytomegaloviral and other GPR proteins. The receptor proteins were used to design polypeptides, pref. based on the transmembrane domains, for use in G-protein coupled receptor ligand binding assays. The polypeptide fragments retain biological activity such as binding a GPR ligand or modulating GPR ligand binding to a GPR (see AAW02741-W0299) for examples of polypeptide fragments). The polypeptide fragments can be used in compositions for treating subjects suffering

Column

69-72; 184pp; English.

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RESULT 12
ABU67205
ID ABU67
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Best Local
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comprising an NPXXY motif, and a carboxyl terminal tail which comprises a putative site of palmitoylation and clusters of phosphorylation, and a retained portion of a carboxyl terminal region of a GPCR portion fused to phosphorylation of the carboxyl terminal from a second GPCR, that comprises phosphorylation clusters and a putative palmitoylation site 10-25 amino acid residues downstream of a second NPXXY motif. The modified GPCR is useful for screening compounds for GPCR activity which comprises providing a cell that expresses at least one modified GPCR, where the cell further comprises arrestin conjugated to a detectable molecule, exposing the cell to the compound, detecting the location of the arrestin within the cell, comparing the location of the arrestin within the cell to the compound to the location of the arrestin within the cell to the compound to the location of the arrestin within the cell to the compound to the location of the arrestin within the cell to the compound to the location of the arrestin within the cell to the compound to the location of the arrestin within the cell to the compound to the location of the arrestin within the cell to the compound to the location of the arrestin within the cell to the compound to the location of the arrestin within the cell to the compound to the location of the arrestin within the cell to the compound to the location of the arrestin within the cell to the compound to the location of the arrestin within the cell to the compound to the location of the arrestin within the cell to the compound to the location of the arrestin within the cell to the compound to the location of the arrestin within the cell to the compound to the location of the arrestin within the cell to the compound to the location of the arrestin within the cell to the compound to the location of the arrestin within the cell to the compound to the location of the arrestin within the cell to the compound to the location of the arrestin within the cell to the carbox within the cell to the carbo
                                                                                                                                                                                                                                                                                                                                                       Modified G-protein coupled receptor useful for identifying inverse agonist or antagonist of the receptor, comprises a terminal having one or more clusters of phosphorylation -
                                                                                                                                                                                                                                                                               The invention
                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 2; 57pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-690758/74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oakley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; G-protein coupled receptor; receptor; GPCR; palmitoylation site; phosphorylation cluster; arrestin; endosome; angina pectoris; rhinitis; atherosclerosis; asthma; emphysema; inflammatory disease; glaucoma; pain; rheumatoid arthritis; obesity; Parkinson's disease; rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-NOV-2000; 2000US-245772P.
08-JAN-2001; 2001US-260363P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G-protein coupled receptor (GPCR) fragment #4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BARA/)
(LAPO/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-NOV-2001; 2001US-0993844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Updated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a pathology related to as schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BARAK L S.
LAPORTE S A.
CARON M G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OAKLEY R H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barak LS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                330 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003 to
                                                                                                                                                                                                                                           relates to a modified G-protein coupled receptor (GPCR) NPXXY motif, and a carboxyl terminal tail which compris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laporte
                                                                                                                                                                                                                                                                                                                         English.
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Pred. No. 2.7e-101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPR abnormality e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caron MG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D
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                                                                                                                                                                                                                                                                                                                                                                              an agonist, carboxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163
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RESULT 13
ABP53986
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Best Local S
Matches 29
The present invention describes a method for detecting G protein-coupled receptor (GPCR) pathway activity. The method comprises: (1) providing at least one cell expressing GPCR and conjugated proteins; (2) treating the cell with a test compound; (3) obtaining a digital image of the cell by detecting and measuring energy emitted from the detectable molecules; and (4) detecting the localization of some of the conjugated proteins at one of endocytic vesicles and endosomes. The method can be used for detecting compounds that activate GPCR-activity in vivo and in vitro, where the including photo-transduction, olfaction, neurotransmission, vascular come, cardiac output, digestion, pain and fluid electrolyte balance. The present sequence represents a GPCR amino acid sequence which is given
                                                                                                                                                                                                                                                                          Detecting G-protein-coupled receptor pathway activity comprises treating a cell having G-protein-coupled receptor activity with a test compound, obtaining a digital image of the cell and detecting position
                                                                                                                                                                                                                                 Disclosure; Page 24; 42pp; English.
                                                                                                                                                                                                                                                                     of conjugated proteins
                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-018747/01.
                                                                                                                                                                                                                                                                                                                                                                                         Barak LS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the cell in the absence of the compound and correlating a difference between the location of arrestin within the cell in the presence of the compound and the presence of the location of the arrestin within the cell in the absence of the compound. Preferably, the arrestin is detected in endosomes. The GPCR and a nucleic acid encoding the modified GPCR are useful for preventing and/or treating a disease associated with GPCR in mammals, such as angina pectoris, atherosclerosis, asthma, emphysema, rhinitis, inflammatory disease, rheumatoid arthritis, glaucoma, pain, obesity or Parkinson's disease, by modulating GPCR activity and affinity for arrestin. Sequences ABU67202-ABU67240 represent GPCR polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                        (UYDU-) UNIV DUKE
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12-MAR-2002; 2002US-0095620.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               digestion; pain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               photo-transduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human alpha 2B adrenergic receptor class A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein-coupled receptor; GPCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 419 NPVIYTIFNQDFRRAFRRILCRPWTQTAW 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                      Oakley RH;
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The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (I)-(III) by detecting a polymorphic site, comprising; (a) obtaining a sample having a polymorphic serie, comprising; alpha2A or alpha2C or fragment or complement of; and (b) detecting a polymorphic site comprising nucleotide positions 901-909 of (I), a site comprising cytosine or guanine at position 753 of (IIV) or a site comprising (A) (99996999050) or (B) (999969918) or (B) (999969918) or a positions 961-972 of (III). The method may be used for genotyping an alpha2B, alpha2A or alpha2C receptor gene and further used to determine whether an individual is at increased risk of developing a disease associated with alpha2B, alpha2A or alpha2, comprising detecting a polymorphic site which correlate to disease selected from cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-APR-2000;
10-AUG-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                       determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity; phosphorylation; inositol phosphate; alpha-2CAR.
                                                                                                                                                                                                                                                                                                                                                           Claim 78; Page 160-162; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liggett
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Matches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          drugs.
                                               ARQ64890 encodes the amino acid sequence of a polypeptide (ARR54834) that constitutes human derived adrenaline alpha 2CII receptor. The DNA can be used for the study of the pharmacological importance of the gene expression in humans.
                                                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                 screening
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                                                                                                                                                                                                                                                         Adrenaline receptor
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                                                                                                                                                                            Page 9-11; 13pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VYLALDVLFCTSSIVHLCAISLDRYW 112
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to the alpha 2CII receptor
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Search completed: February 6, 2004, 18:23:32 Job time : 38.3746 secs
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                                                                                    87 VYLALDVLPCTSSIVHLCAISLDRYW 112
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RESULT 1
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US-08-194-338-4
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US-07-741-453A-46
US-08-118-270-21
PCT-US93-08528-21
US-08-18-5
US-08-194-338-5
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US-08-118-270-22
                                                                                                            ALIGNMENTS
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Application US/08118270

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RESULT 2
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                                                                                                                                                                                                                                                                                          Sequence 20, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND ME
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local Similarity
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PseentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION NUMBER: US 07/943,236
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSEND: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2A
TELECOMPUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 5508384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Schuster, David I.

TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN

TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF

NUMBER OF SEQUENCES: 348

CORRESPONDENCE ADDRESS:

ADDRESSER: DOCUMENTS OF GRAPH OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF 
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 1: MOLECULE TYPE:
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TELEFAX: 248633
                                                                                                                              STATE: I
                                                                                                                                                                                                                             STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 419 Sever CITY: Washington
                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104
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                                                                                                      20004
                                                                                                                                                                                              Washington
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                                                                                                                                                                D.C.
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                                                                                                                                                                                                                                E: BROWDY AND NEIMARK
419 Seventh Street, N
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419 Seventh Street, N.W.,
                                                                                                                                 USA
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                                                                                                                                                                                                                             Street,
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                                                                                                                                                                                                                                N.W.,
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                                                                                                                                                                                                                                    Suite 300
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RESULT 3
US-08-194-338-4
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                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: TETRALITY NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE NUMBER: TOTALE N
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GENERAL INFORMATION:
APPLICANT: Venter, John C.
APPLICANT: Fraser, Claire M.
APPLICANT: MCCombie, William R.
TITLE OF INVENTION: OCTOPAMINE RECEPTOR
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NAME: ISTAELSEN, NEd A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH101.001DV1
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, olson and Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
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                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 08-FE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: UZIP: 92660
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REFERENCE/DOCKET NUMBER: MU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
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PRIOR APPLICATION NUMBER: US 07/943,236
PRIOR APPLICATION NUMBER: 10-SEP-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4, Application US/08194338
5. 5474898
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N: 435
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                                                                                                                                                                                                         US 07/676,174
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n Release #1.0, Version #1.25
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US-08-103-170-17
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TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
      Query Match
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                                                       MOLECULE TYPE: p
FRAGMENT TYPE: i
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.8%; Score 26; DB Best Local Similarity 100.0%; Pred. No. 1. Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                              NAME: Lavalleye, Jean-Paul
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521,4500
                                                                                                                                                                                                                                                                                CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 07
PTITING DATE: 24-DEC-1990
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1755
CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                         ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gantz, II
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 VYLALDVLFCTSSIVHLCAISLDRYW 151
                                                                                                   amino acid
XGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7, Application US/08103170
5885824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1755 Jefferson Davis Highway, Fourth Floor
                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamada, Tadataka
Gantz, Ira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ະວະ: single
linear
                                                                       internal
                                                                                     peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          internal
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5.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant Genomic Clones Encoding
Histamine H1, H2, and H3 Receptors, Met
Thereof, and Proteins Encoded Therefrom
                                                                                                                                                                                                                                                                                               US 07/633,060
                                                                                                                                                                                                                                                                                                                                                       US/08/103,170
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Score 25;

DB 2

Length 27;

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US-08-118-270-21
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                                                                                                                                                                         RESULT 6
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US-07-741-453A-46
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                                                                                                                                                                                                                                                                                                                                                                 US-07-741-453A-46
                                                                                                                     Sequence 21, Application US/08118270 Patent No. 5508384
                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 46, Application US/07741453A
                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
              APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/741,453A
FILING DATE: 19911015
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 56 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: VASSART, GILBERT
TITLE OF INVENTION: POLYPEP1
TITLE OF INVENTION: ACTIVITY
TITLE OF INVENTION: AND POLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Disk
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 6
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                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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                                                                                                                                                                                                                                          88 YLALDVLFCTSSIVHLCAISLDRYW 112
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                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (202) 861-3000
                                                                                                                                                                                                                                                                                                                                                                               peptide
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                                                                                                                                                                                                                                                                                                         5.6%;
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                                                                                                                                                                                                                                                                                                           Score 25; Pred. No.
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Best Local Similarity 100.0%;
Matches 25; Conservative (
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INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943
PILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSERD, KEVIN G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: WIRP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSEND, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MUI
                                                                      APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                   STREET: 419 Seven
                                                                                                                                                                                                                                                                                ZIP: 20004
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STRANDEDNESS: sir
TOPOLOGY: linear
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TELEPHONE: 202-737-3528
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STREET: 419 Seventh Street, N.W., Suite 300
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                                                                                                                                                                                                                                                                                                                       D.C.
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                                                                                                                                                                                                                                                                                                                                                          419 Seventh Street, N.W., Suite 300
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 MURPHY=2 PCT
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US-08-465-971B-4
                                                                            Matches
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US-08-465-971B-4
                                                                                                          Query Match
                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WOXIDPERFECT 5.1
CURRENT APPLICATION APATA:
APPLICATION NUMBER: US/08/465,971E
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: WULLINS, J.G.
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 325800-4:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 4:
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                           TYPE: amino acids
STRANDEDNESS: not releva
TOPOLOGY: not relevant
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Human G-Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 202-628-5197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single TOPOLOGY: linear
112 YLALDVLFCTSSIVHLCAISLDRYW 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                     88 YLALDVLFCTSSIVHLCAISLDRYW 112
                                                                            25;
                                                             h 5.6%; Score 25; DB 2; I
Similarity 100.0%; Pred. No. 7.4e-13;
25; Conservative 0; Mismatches 0;
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1 Similarity 100.0%;
25; Conservation
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amino acid
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E: Cecchi, Stewart & Olstein
6 Becker Farm Road
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                                                                                                                                                                                       not relevant
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                              Length 358;
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                                                           0,
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RESULT 9

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US-08-196-989B-11
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                                                                                                                                                                                      Sequence 11, Application US/08196989B
Patent:No. 5585476
GENERAL INFORMATION:
APPLICANT: MacLennan, A. John
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 9:
Matches 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,174
PILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH101.001
TELECOMMUNICATION INFORMATION:
TRIEBHONE: (470) 73F-DEFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (619) 235-01
COMPUTER READABLE FORM:
                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: 1
ANTI-SENSE: NO
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Venter, John C.
APPLICANT: Fraser, Claire M.
APPLICANT: MCCombie, William R.
TITLE OF INVENTION: OCTOPAMINE RECEPTOR
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Knobbe, M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELEPHONE:
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                                                                                                                                                                                                                                                                                                                                      88 YLALDVLFCTSSIVHLCAISLDRYW 112
                   32606
                                                                  Gainesville
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T: 620 Newport Center Drive, Sixteenth Floor
Newport Beach
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                                                                                                                                                                                     MacLennan,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
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                                                                                                                                           Molecular Cloning
G-Protein Coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235-8550
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                                                                                                                                        and Expression of Receptors
                                                                                                                                                                                                                                                                                                                                                                                               DB 1; I
. 9.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                              Length 450
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OPERATING SYSTEM:

IBM PC compatible SYSTEM: PC-DOS/MS-DOS MEDIUM TYPE:

Floppy disk

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US-08-444-734A-8
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                                                    SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,734A
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/029,917
FILING DATE: 03-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/548,714
PILING DATE: 03-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/548,714
FILING DATE: 06-JUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 56102
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/196,989B
FILING DATE: 15-FEB-1994
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: cDNA encoding the rat D1 dopamine
TITLE OF INVENTION: receptor linked to adnylyl cyclase activation and
TITLE OF INVENTION: expression of the receptor protein in plasmid-transfected
TITLE OF INVENTION: cell lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 5.6%; Score 25; DB
Local Similarity 100.0%; Pred. No. 9.
hee 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
               NAME: Altman, Daniel E. REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: not
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
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Mahan, Lawrence C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sibley, David R.
                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       not relevant
NIH065.001FW1
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US-08-760-936-11
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                                            Matches
                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                          TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: MacLen
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,936
FILING DATE: December 6, 1996
CLASSIFICATION: 536
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                           TOPOLOGY: no
                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 352-375-8100
                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Pace, Dotan R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Molecular Cloning and Expression TITLE OF INVENTION: G-Protein Coupled Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 2421 N.W. CITY: Gainesville
                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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TOPOLOGY: linear
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88 YLALDVLFCTSSIVHLCAISLDRYW 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 YLALDVLFCTSSIVHLCAISLDRYW 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MacLennan, A. John
                                            Conservative
                                                                                                                             not relevant
3: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saliwanchik,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                not relevant
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100.0%; Pred. No. 9.1e-13;
                                                           5.6%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lloyd & Saliwanchik
                                                          Score 25; ; Pred. No.
                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                          Mismatches
                                                                             DB 2;
                                                             9.1e-13
                                                                        Length 450;
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                                            Gaps
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US-08-118-270-332
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US-09-225-024-11
                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                                      Sequence 332, Application US/08118270 Patent No. 5508384
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/09225024 Patent No. 6518414
                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 352-372-5800 INFORMATION FOR SEQ ID NO: 11:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acids
STRANDEDNESS: not relevant
TOPOLOGY: not
                                                                  NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AN
                                                                                                                    APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Pace, Doxan R.
REGISTAN NUMBER: 38,261
REFERENCE/DOCKET NUMBER: MA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,936
FILING DATE: 6-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/196,989
FILING DATE: 15-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Molecular Cloning and Expression of TITLE OF INVENTION: G-Protein Coupled Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MacLennan, A. John
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                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
hes 25; Conservative
COUNTRY:
                                                    STREET:
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                                                  E: BROWDY AND NEIMARK
419 Seventh Street, N.W.,
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2421 N.W. 41st Street, Suite A-1
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100.0%; Pred. No. 9.1e-13
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PCT-US93-08528-332
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TELEX: 248633
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                       REFERENCE/DOCKET NUMBER: MUR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPAX: 202-777
                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PROPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REGISTRATION NUMBER: MURPHY=2A
                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
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PILING DATE: 09-SEP-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP-SEP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 248633
                                                                                                             NAME: Townsend, Kevin REGISTRATION NUMBER: 3
                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 419 Sever
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419 Seventh Street, N.W., Suite 300
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Pred. No.
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1: /cgn2_6/ptcdata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptcdata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptcdata/1/pubpaa/US06_PUBCOMB.pep:*

4: /cgn2_6/ptcdata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptcdata/1/pubpaa/US07_NEW_PUB.pep:*

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1 MDHQDPYSVQATAA
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US-10-001-073-8

US-9-825-923-4

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US-10-001-073-7

US-10-001-073-4

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Compugen Ltd
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Sequence 12, Appli
Sequence 18, Appl
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Sequence 44, Appl
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US-09-825-923-2
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Minimum

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Title: Perfect score:

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## ALIGNMENTS

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; LENGTH: 447
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US-09-825-923-2
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APPLICANT: Heinonen, Paula
APPLICANT: Alhopuro, Matti
APPLICANT: Karyonen, Matti
APPLICANT: Koulu, Markku
APPLICANT: Pesonen, Ullamari
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Best Local Similarity 100.0%;
Matches 447; Conservative 0
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 2
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APPLICANT: Salonen, Riitta
APPLICANT: Salonen, Riitta
APPLICANT: Kauhanen, Jussi
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
ENTAREN FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 NSKRIPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGS 180
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Scheinin, Mika
Salonen, Jukka T
Tuomainen, Tomi-Pekka
Lakka, Timo A
VIYTIFNQDFRRAFRRILCRPWTQTAW
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                                                                                                                TREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPKHCKVPHGLFQFFFWIGYCNSSLNP 420
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                                                                                  TREKRETEVLAVVIGVEVLCWPPFFFSYSLGAICPKHCKVPHGLFOFFFWIGYCNSSLNP
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RESULT 3
US-10-001-073-8
US-10-001-073-8
; Sequence 8, Application US/10001073
; Publication No. US20030113725A1
; GENERAL INFORMATION:
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Publication No. US2003003470A1
GENERAL INFORMATION:
APPLICANT: Salonen, Jukka T
ITILE OF INVENTION: Method for detecting a r
FILE REFERENCE: 0933-0183p
CURRENT APPLICATION NUMBER: US/10/077,870
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: FI 20010323
PRIOR PILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 3.1
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-077-870-2
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             APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
        SOFTWARE: PatentIn Ver.
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Best Local Similarity 100.0%;
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; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo 6
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Best Local Similarity
Matches 447; Conser
421 VIYTIFNODFRRAFRRILCRPWTQTAW 447
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APPLICANT: Kauhanen, Jussi
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a var
TITLE OF INVENTION: protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
SOFTWARE: PatentIn Ver. SEQ ID NO 4
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APPLICANT: Snapir, Amir
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Patent No. US20010016338A1
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Alhopuro, Pia
Karvonen, Matti
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Nyyss"nen, Kristiina
Salonen, Riitta
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Scheinin, Mika
Salonen, Jukka T
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Matches 306
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Best Local Similarity
Matches 306; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Salonen, Jukka T
TITLE OF INVENTION: Method for detecting a risk of hypertension and
FILE REFERENCE: 0933-0183P
CURRENT APPLICATION NUMBER: US/10/077,870
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: FI 20010323
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 3.1
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                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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100.0%; Pred. No. 2.6e-252;
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Sequence 42, Application US/1022567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: ROUBH, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTITILE OF INVENTION NUMBER: US/10/225,567A
CURRENT APPLICATION NUMBER: US/10/257,144
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR PILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-001-073-7
                                                                                                                                                                                                                                                                                   RESULT 7
US-10-225-567A-42
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US-10-001-073-7
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Publication No. US20030113725A1
PREFEAL INFORMATION:
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Best Local
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APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                           ANTIBODIES
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CURRENT APPLICATION NUMBER: US/09/993,844
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: US 60/245,772
PRIOR FILING DATE: 2000-11-03
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-08
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 29
TYPE: PRT
       ; Sequence 46,
                       RESULT 9
US-10-001-073-46
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Best Local Similarity
Matches 29; Conserv
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APPLICANT: Barak, Lawrence S.
APPLICANT: Laporte, Stephane A.
APPLICANT: Caron, Marc G.
TITLE OF INVENTION: Modified G-Protein Coupled Receptors
FILE REFERENCE: 033072-026
                                                                                                                                                                                                                                               ORGANISM: Human
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Best Local Similarity
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ORGANISM: Homo sapiens
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                                                                                  NPVÍYTÍFNODFRRÁFRRÍLCRÞWTOTÁW 29
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Application US/10001073
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                                                                                                                                                6.5%; Score 29; DB 10;
100.0%; Pred. No. 2.6e-17;
tive 0; Mismatches 0
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100.0%; Pred. No. 2.6e-252;
vative 0; Mismatches 0; Indels
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; Publication No. US20030113725A1
; GRMERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kirsten
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCT;
; CURRENT APPLICATION UNMBER: US/10/001,073
; CURRENT FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 46
LENGTH: 458
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US-10-001-073-44
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LENGTH: 462
TYPE: PRT
                                          Sequence 44, Application US/10001073
Publication No. US20030113725A1
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER: OF:SEQ ID NOS: 2292
SOCTWARE: Patentin version 3.1
FENOTRE: Patentin version 3.1
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; ORGANISM: Homo sapiens
US-10-001-073-46
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Publication No. US20030113798A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Pred. No. 9e-14;
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GENERAL INFORMATION:

APPLICANT: Liggett, Stephen

APPLICANT: Small, Kirsten

ITILE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms

FILE REFERENCE: 13073-PCT

CURRENT FILING DATE: 2001-11-01

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PATENTION VET. 2.0

SEQ ID NO 26

LENGTH: 450

TYPE: PRT

ORGANISM: Homo sapiens

US-10-001-073-26
                                            RESULT 14
US-10-225-567A-40
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US-10-001-073-44
                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 27
LENGTH: 450
Sequence 40, Application US/10225567A Publication No. US20030113798A1 GENERAL INFORMATION:
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Best Local Similarity
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ORGANISM: Homo sapiens
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Best Local Similarity 100.0%;
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CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109
                                                                                                                109 YLALDVLFCTSSIVHLCAISLDRYW 133
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100.0%; Pred. No. 6.3e-13;
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; Pred. No. 9.1e-14;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-40
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                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 07/273373
PRIOR FILING DATE: 1989-11-18
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
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                                                                         Matches
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                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bunzow, James R.
APPLICANT: Grandy, David K.
APPLICANT: Machida, Curtis A.
TITLE OF INVENTION: Dopamine Receptors and Genes
FILE REFERENCE: 90-1092-CCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR PILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Civelli Olivier
APPLICANT: Bunzow, James I
APPLICANT: Grandy, David I
APPLICANT: Machida, Curtii
                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 07/973588
PRIOR FILING DATE: 1992-11-09
PRIOR APPLICATION NUMBER: 07/438544
PRIOR FILING DATE: 1989-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/238977 PRIOR FILING DATE: 1999-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/060,795B
CURRENT FILING DATE: 2002-01-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: LifeSpan Biosciences APPLICANT: Brown, Joseph P.
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 08/474892
PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                        LENGTH:
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109
                 88 YLALDVLFCTSSIVHLCAISL 108
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                                                                       Conservative
                                                                                             100.0%;
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; Pred. No.
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Search completed: February 6, 2004, 18:28:04 Job time : 30.4013 secs

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# GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model Run on: February 6, 2004, 18:20:56 ; Search time 16.4448 Seconds (without alignments) 2614.040 Million cell updates/sec

Title: US-09-692-077D-8
Perfect score: 447
Sequence: 1 MDHQDPYSVQATAAIAAAIT..

.QDFRRAFRRILCRPWTQTAW

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

96168682 residues

Searched: 283308 seqs, Word size : 20

Total number of hits satisfying chosen parameters:

16

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

PIR\_76:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

#### SUMMARIES

16	15	14	13	12	11	10	9	8	7	თ	տ	4	w	N	_	Regult No.
25	25	25	25	25	25	26	26	26	26	26	63	71	71	176	306	Score
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450	450	450	450	450	432	461	458	458	458	458	453	455	448	276	450	Length
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I49481	A34169	JH0190	B40392	A38316	I50829	A31237	I49480	A37869	A40392	A48392	A35642	S28221	I51883	I53161	A37223	ID
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## ALIGNMENTS

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RESULT 2 I53161 alpha 2-adrenergic receptor,

islets of Langerhans -

rat

(fragment)

A;Molecule type: DNA
A;Residues: 56-185 <CCHI>
A;Cross-references: GB:X59684; NID:g28635
A;Cross-references: GB:X59684; NID:g28635
A;Note: this translation is not annotated in GenBank entry HS
R;Chang, A.C.; Ho, T.F.; Chang, N.C.
Biochem. Biophys. Res. Commun. 172, 817-823, 1990
A;Title: In vitro amplification by polymerase chain reaction
A;Reference number: A36158; MUID:91054503; PMID:2173582
A;Accession: A36158 A;Gene: GDB:ADRA2B; ADRARL1; ADRA2L1; ADRA2RL1
A;Cross-references: GDB:120539; OMIM:104260
A;Map position: 2p13-2q13
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycopi R;Lomasney, J.W.; Lorenz, W.; Allen, L.F.; King, K.; Regan, J. Proc. Natl. Acad. Sci. U.S.A. 87, 5094-5098, 1990
A;Title: Expansion of the alpha 2-adrenergic receptor family: A;Reference number: 139407; MUID:90311349; PMID:2164221
A;Accession: 139407 A,Title: Cloning, expression, and pharmacological characterization A;Reference number: A37223; MUID:91042469; PMID:2172775 A;Accession: A37223 Ş 문 ঠ 문 S 문 Ś 밁 ð 밁 A;Molecule type: DNA A;Residues: 95-361,'QL',364-389 <CHA> A;Cross-references: GB:M38742; NID:g177867; PIDN:AAA62823.1; PID:g177868 A,Cross-references: GB:M34041; NID:g178197; PIDN:AAA51666.1; PID:g178198 R;Chhajlani, V.; Rangel, N.; Uhlen, S.; Wikberg, J.E.S. FEBS Lett. 280, 241-244, 1991 A;Status: preliminary FEBS Lett. 280, 241-244, 1991
A;Title: Identification of an additional gene belonging A;Reference number: S14308; MUID:91192139; PMID:1849485
A;Accession: S14308 A; Molecule type: DNA A; Residues: 1-450 < LOM> A;Status: preliminary A;Residues: 1 A; Molecule type: DNA A; Status: nucleic acid sequence not shown; not compared with conceptual translation Mol. Pharmacol. 38, 681-688, 1990 Query Match Matches Local Simhes 306; 301 241 241 181 181 121 121 NSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGS 301 5 13  $\vdash$ 1 MDHQDPYSVQATAAIAAAITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADIL 60 Similarity NSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGS VATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEY VATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEY 120 EEEEEE 306 ASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEEE ASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGOGOKEGVCGASPEDEAEEE 300 FFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALASV FFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALASV MDHQDPYSVQATAAIAAAITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADIL 60 EEEEEE 306 ilarity 100.0%; I Conservative 0; 68.5%; Score 306; DB 2; Lo 100.0%; Pred. No. 3.2e-289; Live 0; Mismatches 0; receptor; glycoprotein; transmembrane Length 450 Indels ö HSALPH218, the alpha(2) adrenergic J.W.; Yang-Feng, T.L.; Caron 0f cloning and a partial 0, of a human alpha-2B-ac protein Gaps release gene encoding characterization 180 180 120 300 240 240 111.0 recep

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alpha-2-C2 adrenergic receptor - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 13-Aug-1999 C;Accession: S28221, JH0693 R;Chen, W.M.; Chang, A.C.; Shie, B.J.; Chang, Y.H.; Chang, N.C.A. Biochim. Biophys. Acca 1171, 219-223, 1992 A;Title: Molecular cloning and characterization of a mouse alpha(2)C2 adrenoceptor subty, A;Reference number: S28221, MUID:93129625; PMID:1336396
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C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alpha-2B-adrenergic receptor - rat
(;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Uul-1996 #sequence_revision 26-Jul-1996 #text_change 13-A
C;Accession: I5183
R;Le Jossec, M.; Cloix, J.F.; Pecquery, R.; Giudicelli, Y.; Dausse,
Am. J. Hypertens. 8, 17-182, 1934
Am. J. Hypertens. 8, 17-182, 1934
A;Title: Differential sodium regulation between salt-sensitive and salt-seroce number: I51883; MUID:95275492; PMID:7755946
A;Recession: I51883
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residnes. 1-448, DEC.
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C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_
C;Accession: I53161
R;Wang, S; X; Pilkey, D.T.
Diabetes 43, 127-136, 1994
A;Title: Identification in islets of Langerhans of a new
A;Reference number: I53161; MUID:94085695; PMID:8262309
A;Accession: I53161
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Matches 71
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3. 1.2e-60;

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                RESULT 6
A48392
alpha 2C4 adrenoceptor subtype - mouse
N;Alternate names: alpha 2C4 isoceptor
C;Species: Mus musculus (house mouse)
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alpha-2B-adrenergic receptor - rat C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
C;Accession: A35642
R;Zeng, D; Harrison, J.K.; D'Angelo, D.D.; Barber, C.M.; Tucker, A.L.; Lu, Proc. Natl. Acad. Sci. U.S.A. 87, 3102-3106, 1990
A;Title: Molecular characterization of a rat alpha-2B-adrenergic receptor. A;Reference number: A35642; MUID:90222177; PMID:2158103
A;Accession: A35642; MUID:90222177; PMID:2158103
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                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-453 <ZEN>
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A;Note: the authors translated the codon CCA for residue 161 as Phe, ACT for residue 33
A;Note: the authors translated the codon CCA for residue 161 as Phe, ACT for residue 33
R;Chruscinski, A.J.; Link, R.E.; Daunt, D.A.; Barsh, G.S.; Kobilka, B.K.
Biochem. Biophys. Res. Commun. 186, 1280-1287, 1992
A;Title: Cloning and expression of the mouse homolog of the human alpha2-C2 adrenergic A;Reference number: JH0693; MUID:92378586; PMID:1354956
A;Accession: JH0693
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A; Residues: 6-228, 231-455 < CHR >
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-455 <CHE>
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                                                                                    23 AITFLILFTIFGNALVILAVLTSRSLRAPONLFLVSLAAADILVATLIIPFSLANELLGY
                                                                                                                   18 AITFLILFTIFGNALVILAVLTSRSLRAPONLFLVSLAAADILVATLIIPFSLANELLGY
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                                                 WYF 80
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85
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100.0%; Pred. No.
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C; Date: 19-Nov-1993 #
C; Accession: A48392
R; Chang, Y.H.; Chang,
Biochem. Mol. Biol. I
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J. Biol. Chem. 266, 10470-10478, 1991
A;Title: Isolation of rat genomic clones encoding subtypes of the alpha-2-adrenergic rec A;Reference number: A40392; MUID:91244823; PMID:1645350
A;Accession: A40392
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-458 <LAN>
A;Residues: 1-458 <LAN>
A;Residues: 1-458 <LAN>
A;Cross-references: GB:M62371; NID:9206612; PIDN:AAA42033.1; PID:9206613
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alpha-2-adrenergic receptor (clone RG10) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Dec-1991 #sequence_revision 03-Apr-1
C;Accession: A40792
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A;Title: Molecular characterization of a murine homologue A;Reference number: A48392; MUID:93250567; PMID:8387367
A;Accession: A48392
A;Cross-references: GB:M58316; NID:g202585; PIDN:AAA40634.1; PID:g202586
A;Note: the authors translated the codon ACC for residue 69 as Asn and GCG for residue 8
R;Voigt, M.M.; McCune; S.K.; Kanterman, R.Y.; Felder, C.C.
FEBS Lett. 278, 45-50, 1991
A;Title: The rat alpha(2)-C4 adrenergic receptor gene encodes a novel pharmacological su
A;Reference number: S13023; MUID:91130596; PMID:1704314
A;Recession: S13023
                                                                                                                                                                    R;Flordellis, C.S.; Handy, D.E.; Bresnahan, M.R.; Zannis, V.I.; Gavras, H. Proc. Natl. Acad. Sci. U.S.A. 88, 1019-1023, 1991
A;Title: Cloning and expression of a rat brain alpha-2B-adrenergic receptor A;Reference number: A37869; MUID:91126047; PMID:1704126
A;Accession: A37869
A;Molecule type: mRNA
A;Residues: 1-458 <FLO>
A;Residues: 1-458 <FLO>
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A;Experimental source: DBA/Z, liver
A;Note: sequence extracted from NCBI backbone (NCBIN:131475, NCBIP:131476)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                     alpha-2B-adrenergic receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
C;Accession: A37889; S13023
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A;Molecule type: nucleic acid
A;Residues: 1-458 <CHA>
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Pred. No.
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6.9e-17;
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A;Map position: 4p16.3-4p15
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor;
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                                                                                                                                                                                                                                                                                                                                                                          R;Chhajlani, V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Regan, J.W.; Kobilka, T.S.; Yang-Feng, T.L.; Caron, M.G.; Lefkowitz, R.J.; Kobilka, B.! Proc. Natl. Acad. Sci. U.S.A. 85, 631-6305, 1988
A;Title: Cloning and expression of a human kidney cDNA for an alpha-2-adrenergic recepto: A;Reference number: A31237; MUID:88320430; PMID:2842764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: GDB:ADRA2C; ADRARL2; ADRA;Cross-references: GDB:120540;
                                                                                                                                                A; Molecule type: DNA
A; Residues: 95-223 < CH2 >
                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
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A;Tille: Cloning of two mouse genes encoding alpha-2 adrenergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: I49480
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                                                                                                                                                                                                    A; Accession: S14310
                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 95-223 < CHH>
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A; Residues: 1-461 < REG>
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C;Superfamily: vertebrate rhodopsin
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A;Reference number: 149480; MUID:92342131; PMID:1353249
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ntive 0; Mismatches
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100.0%; Pred. No. 6.9e-1
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10; OMIM:104250
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Pred. No.
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transmembrane protein

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alpha-2-adrenergic receptor (clone RG10) - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 06-Dec-1991 #sequence_revision 03-Apr-1992 #text_change C;Accession: B40392 R;Lanier, S.M.; Downing, S.; Duzic, E.; Homcy, C.J. J. Biol. Chem. 266, 10470-10478, 1991 A;Reference number: A40392; MUID:91244823; PMID:1645350
                                                                                                                                                                      RESULT 13
B40392
                                                                                                                                                                                                                                                                                                                                                                                                                           alpha-2-adrenergic receptor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
C;Accession: A38316
R;Guyer, C.A.; Horstman, D.A.; Wilson, A.L.; Clark, J.D.; Cragoe Jr., E.J.; Limbird, L.E
J. Blol. Chem. 265, 17307-17317, 1990
A;Title: Cloning, sequencing, and expression of the gene encoding the porcine alpha-2-ad
A;Reference number: A38316; MUID:91009167; PMID:2170371
A;Accession: A38316
A;Accession: A38316
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C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane prot
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A38316
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A;Title: Cloning and expression of a fish a2-adrenoceptor. A;Reference number: I50829; MUID:94035926; PMID:7693288
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alpha 2-adrenoceptor - cuckoo wrasse
C;Species: Labrus ossifagus (cuckoo wrasse)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 13-Aug-1999
C;Accession: I50829
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A;Status: prelimina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Le
                                                                                                                                                                                                                                                                                                                     6.4e-16;
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                                                                                                                                                                                                                                                                                                                                       Length 450;
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               of the alpha-2-adrenergic
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                                                                                         13-Aug-1999
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                                                                                                                                                                                                                                                                                                   0,
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F;34-59/Domain: hydrophobic <HDI>
F;71-96/Domain: hydrophobic <HII>
F;106-131/Domain: hydrophobic <HII>
F;150-175/Domain: hydrophobic <HIV>
F;159-218/Domain: hydrophobic <HV>
F;193-218/Domain: hydrophobic <HV>
F;193-400/Domain: hydrophobic <HVI>
F;405-430/Domain: hydrophobic <HVI>
                                                                                                                                                                                                                                                                                       C; Superfamily: vertebrate
C; Keywords: G protein-cour
                                                                                                                                                                                                                                                                                                   C; Comment: Alpha-2-adrenergic receptor is a predominant catecholamine receptor. It
                                                                                                                                                                                                                                                                                                                                                                                                C)Access, Duga, ..., 17
R;Chalberg, S.C.; Duga, ..., 17
Mol. Cell. Biochem. 97, 161-17
Mol. Cell. Biochem. 97, 161-17
A;Title: Molecular cloning, so
A;Title: Molecular cloning, so
                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-450 <CHA>
A;Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A; Accession: JH0190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Feb-1997
C;Accession: JH0190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alpha-2-adrenergic receptor - C; Species: Rattus norvariant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Rolecule type: DNA
A;Residues: 1-450 <LAN>
A;FResidues: 1-450 <LAN>
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C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
                                                                                    Matches
                                                                                                      Query Match
Best Local !
                                                                                                                                                                                                                                                                            Keywords: G protein-coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Rattus
109 YLALDVLFCTSSIVHLCAISLDRYW 133
                         88 YLALDVLFCTSSIVHLCAISLDRYW 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 YLALDVLFCTSSIVHLCAISLDRYW 133
                                                                                25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88
                                                                                          Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YLALDVLFCTSSIVHLCAISLDRYW 112
                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Duda, T.; Rhine, J.;
sem. 97, 161-172, 1990
                                                                                                                                                                                                                                                                                                                                                                              mRNA
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                                                                                                                                                                                                                                                                                                 rhodopsin
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                                                                                                                  5.68;
                                                                                                                                                                                                                                                                                                                                                                                                      sequencing and expression of MUID:91125329; PMID:2177834
                                                                      0,
                                                                                            Score 2; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 25; DB; Pred. No. 6.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       J.A.; Sharma, R.K.
                                                                        Mismatches
                                                                                          . No.
                                                                                                                                                                                                                                                                      transmembrane protein
                                                                                            9
                                                                                                            DB 2;
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6.4e-1
                                                                                          .4e-16
                                                                                                        Length 450;
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A;Title: Cloning, sequence analysis, and permanent expression of a human alpha2-adrenery, cyclase attenuation and activation.

A;Reference number: A34169; MUID:89308571; PMID:2568356

A;Accession: A34169

A;Molecule type: DNA
A;Residues: 1-450 <FRA
A;Residues: 1-450 <FRA
A;Cross-references: GB:M23533; NID:g178195; PIDN:AAA51665.1; PID:g178196
A;Kobilka, B.K.; Matsui, H.; Kobilka, T.S.; Yang-Feng, T.L.; Francke, U.; Caron, M.G.;
Science 238, 650-656, 1987

Science 238, 650-656, 1987
                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence revision 22-Jan-1993 #text_change
C;Accession: A34169; A40132; S14311
R;Fraser, C.M.; Arakawa, S.; McCombie, W.R.; Venter, J.C.
J. Biol. Chem. 264, 11754-11761, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A34169
Alba-2A-adrenergic receptor - human
N;Alternate names: alpha-2C10-adrenergic receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                           29-Oct-1999
                                                                                                                                                                                                                                                                                     human alpha2-adrenergs
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밁 5

A;Molecule type: DNA A:Residues: 1-103,'T',105-156,'C',158-367,'L',369-450 <KOB>

A;Title: Cloning, sequencing, and expression of the gene coding for the human A;Reference number: A40132; MUID:88042789; PMID:2823383 A;Accession: A40132

platelet

a) Ĕ

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A;Cross-references: GB:M18415; NID:g17819;.PIDN:AAA51664.1; PID:g178192
A;Note: the authors translated the codon TGT for residue 157 as Val, and CTC for residue
A;Note: part of this sequence was confirmed by protein sequencing
R;Chhaflani, V; Rangel, N.; When, S; Wikberg, J.E.S.
FEBS Lett. 280, 241-244, 1991
A;Title: Identification of an additional gene belonging to the alpha(2) adrenergic receptor; Reference number: $14308; MUID:91192139; PMID:1849485
A;Accession: $14311
A;Molecule type: DNA
A;Residues: 77-123,'p',125-209 <CHH>
C;Genetics:
A;Gene: GDB:ADRA2A; ADRAR; ADRA2R
A;Cross-references: GDB:120538; OMIM:104210
A;Map position: 1025-1025
A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                            밁
Search completed: February 6, 2004, 18:26:08 Job time : 17.4448 secs
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                                                                                                                                     88 YLALDVLFCTSSIVHLCAISLDRYW 112
                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                          0;
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<sup>This</sup> Page Blank (uspto)

Copyright GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd

OM protein - protein search, using sw model

9 February 6, 2004, 18:19:31; Search time 9.96656 Seconds

2109.148 alignments)
Million cell updates/sec

Perfect score: Title: US-09-692-077D-8

Sequence:

Scoring table: Gapop 60.0 , OLIGO Gapext 60.0

MDHQDPYSVQATAAIAAAIT.....QDFRRAFRRILCRPWTQTAW

Searched: 127863 seqs, 47026705 residues

Word size 20

Total number of hits satisfying chosen parameters:

30

Maximum 80 80 seq length: 0 seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution. printed,

## SUMMARIES

71 15.9 455 1 A2AB 63 14.1 382 1 A2AB 63 14.1 386 1 A2AB 63 14.1 387 1 A2AB 62 13.9 389 1 A2AB 62 13.9 392 1 A2AB 62 13.9 397 1 A2AB 62 13.9 397 1 A2AB 62 13.9 397 1 A2AB 62 13.9 397 1 A2AB 62 13.9 397 1 A2AB 62 13.9 397 1 A2AB 62 13.9 397 1 A2AB 62 13.9 397 1 A2AB 63 1 A2AC 64 5.8 458 1 A2AC 65 5.8 458 1 A2AC 65 5.8 462 1 A2AC 65 5.6 450 1 A2AB 65 5.6 450 1 A2AB 65 5.6 450 1 A2AB 65 5.6 450 1 A2AB 65 6 450 1 A2AB 65 6 450 1 A2AB 65 6 450 1 A2AB 65 6 450 1 A2AB 65 6 450 1 A2AB 65 6 450 1 A2AB 65 6 450 1 A2AB 65 6 450 1 A2AB	Regult No.	Score 306 1184 109 100 96 81
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26 5.8 455 1 A2A 26 5.8 458 1 A2A 26 5.8 452 1 A2A 26 5.8 462 1 A2A 26 5.8 469 1 A2A 25 5.6 436 1 A2A 25 5.6 450 1 A2A 25 5.6 450 1 A2A 25 5.6 450 1 A2A 25 5.6 450 1 A2A 25 5.6 450 1 A2A 25 5.6 450 1 A2A 25 5.6 450 1 A2A	17	38
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25 5.6 436 1 A2A 25 5.6 450 1 A2A 25 5.6 450 1 A2A 25 5.6 450 1 A2A 25 5.6 450 1 A2A 25 5.6 450 1 A2A	23	25
25 5.6 450 1 A2A 25 5.6 450 1 A2A 25 5.6 450 1 A2A 25 5.6 450 1 A2A 25 5.6 450 1 A2A	24	25
25 5.6 450 1 A2A 25 5.6 450 1 A2A 25 5.6 450 1 A2A 25 5.6 450 1 A2A	25	25
25 5.6 450 1 A2A 25 5.6 450 1 A2A 25 5.6 450 1 A2A	26	25
25 5.6 450 1 A2A 25 5.6 450 1 A2A	27	25
25 5.6 450 1 A2AJ	28	25
	29	200

ALIGNMENTS

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RESULT 1
A2AB_HUMAN
                                                       entities requires a license agreement (some send an email to license@isb-sib.ch).
                                                                                       between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91054503; PubMed=2173582;
Chang A.C., Ho T.F., Chang N.-C.A.;
Thang A.C., amplification by polymerase chain reaction of a partial
gene encoding the third subtype of alpha-2 adrenergic receptor in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cayla C., Schaak S.,
Submitted (JUL-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning, expression, and pharmacological characterization of a human alpha 2B-adrenergic receptor."; Mol. Pharmacol. 38:681-688(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yang-Feng T.L., Caron M.G., Lerkowitz K.U., "Expansion of the alpha 2-adrenergic receptor family: cloning and characterization of a human alpha 2-adrenergic receptor subtype, t gene for which is located on chromosome 2."; Proc. Natl. Acad. Sci. U.S.A. 87:5094-5098(1990).
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Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Subtype C2).
ADRA2B.
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J. Biol. Chem. 276:4917-4922(2001).
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01-NOV-1990 (Rel. 16, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Small K.M., Brown K.M., Forbes S.L., Liggett S.B.; "Polymorphic deletion of three intracellular acidic residues of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND VARIANT 301-GLU--GLU-303.
MEDLINE=21265012; PubMed=11056163;
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Branchek T.A., Hartig
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Weinshank R.L., Zgombick J.M., Macchi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90311349; PubMed=2164221;
Lomasney J.W., Lorenz W., Allen L.F., King K., Regan J.W.,
Yang-Feng T.L., Caron M.G., Lefkowitz R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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                                                                                                                                                                                                                                                                                                                                            them. Biophys. Res. Commun. 172:817-823 (1990).
FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF GROTEINS. THE RANK ORDER OF POTENCY FOR AGONISTS OF THIS RECEPTOR
M34041;
M38742;
AAA51666.1;
AAA62823.1;
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EMBL; AF316895; AAK01635.1; EMBL; AF005900, AAB62558.1; PIR; A37223; A37223 H8SP; P29274; 1MMH.
Genew; HGNC:282; ADRA2B.

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GO; GO:0005687; C:integral to plasma membrane; TAS.
GO; GO:0007267; P:alpha2-adrenergic receptor activity; TAS.
GO; GO:0007186; P:G-Protein coupled receptor protein signalin. . .; TAS.
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(BY SIMILARITY).
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IMPLICATED IN CATECHOL AGONIST BINDING
(BY SIMILARITY).
(BY SIMILARITY).

MISSING (COMMON POLYMORPHISM; FREQUENCY
IN CAUCASIANS 0.31 AND IN AFRICAN-
AMERICANS 0.12; IMPAIRED PHOSPHORYLATION
AMERICANS 0.12; IMPAIRED PHOSPHORYLATION
PTICEVAR 0.14958.

OL -> HV (IN REF. 1 AND 2).

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MEDIJINE=97357151; PubMed=9214502;

Springer M.S.; Cleven G.C., Madsen O.J., de Jong W.W., Waddell V.G.,

Amrine H.M., Stanhope M.J.;

"Endemic African mammals shake the phylogenetic tree.";

Nature 388:61-64(1997).

-!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-

INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
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019012;
15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)

16-OCT-2001 (Rel. 40, Last annotation update)

16-OCT-2001 (Rel. 40, Last annotation update)

16-OCT-2001 (Rel. 40, Last annotation update)

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16-OCT-2001 (Rel. 36, Last annotation update)
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.
NCBI_TaxID=9365;
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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InterPro; IPR000276; GPCR\_Rhodpsn.

Pfam; PF00001; 7tm\_1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; GPCRTEIN\_RECEP\_F1 ; 1.

PROSITE; PS00237; GPROTEIN\_RECEP\_F1 2; 1.

G-protein coupled receptor; Transmembrane; Multigene family; Phosphorylation; Lipoprotein; Palmitate; Polymorphism.

Phosphorylation; Lipoprotein; Palmitate; Polymorphism.

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CYTOPLASMIC (POTENTIAL)
ASP/GLU-RICH (ACIDIC).
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"Endemic African mammals shake the phylogenetic Nature 388:61-64 (1997).
-I- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIA
                                                                                                                                       PROSITE; PS00237; G PROTEIN RECEP_F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1 2; 1.
G-protein_coupled_receptor; Transmembrane; Multigene family;
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MEDLINE=97357151; PubMed=9214502;
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PRINTS; PR00237; GPCRRHODOPSN
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Mammalia; Eutheria; Tubulidentata; Orycteropodidae;
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            de Jong W.W.,
                                       (POTENTIAL).
                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                             MEDIATE THE CATECHOLAMINE THROUGH THE ACTION OF G
              (POTENTIAL)
                                                                 (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     tree.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
Orycteropus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waddell V.G.,
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RESULT 4
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Best Local
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15-JUL-1999
16-OCT-2001
28-FEB-2003
TRANSMEM
DOMAIN
TRANSMEM
                                                                                                              EMBL; Y16189; CAA76115.1; -.
EMBL; Y15946; CAA75899.2; -.
HSSP; P29274; IMMH.
                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Stanbope M.J., Madsen O.J., Waddell V.G., Cleven G.C., d Stringer M.S., Madsen O.O.M.;

Springer M.S., Madsen O.O.M.;

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE C INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE
                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctola
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DOMAIN
TRANSMEM
DISULFID
DOMAIN
                                  G-protein
                                        PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G_PROTEIN_Coupled receptor; Transmembrane;
                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                      Alpha-2B adrenergic receptor (Alpha-2B ADRA2B.
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                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9986;
                                                                                                  InterPro; IPR000276; GPCR_Rhodpsn
                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                               PROTEINS
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                                                                           PF00001; 7tm 1; 1.
S; PR00237; GPCRRHODOPSN.
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(Rel. 40, Last sequence update)
(Rel. 41, Last annotation updat
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                                                                                                                                                                                                                                                     Integral membrane protein (By similarity).
O FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
2 (POTENTIAL).
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Pred. No.
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IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
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IMPLICATED IN LIGAND BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                              update)
B adrenoceptor) (Fragment).
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1.7e-82;
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                                                                                                                                                                                           as its content is in
                                           Glycoprotein.
                                                                                                                                                                        http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                    Oryctolagus.
                                                                                                                                                                                   Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
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E ACTION OF G
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                                                                                                                                                                                                                   EMBL outstation
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G-protein coupled
Phosphorylation; L
NON TER 1
                                                                        InterPro; IPR000276; GPCR Rhodpsn.

Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRHODDPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS00262; GPROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Transmembrane; Multigene
                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restrance by non-profit institutions as long as its content entities requires a license agreement (See http://www.isb-ecor send an email to license@isb-sib.ch).
                                                                                                                                                                                                   EMBL; Y12525; CAA73125.1; ...
HSSP; P29274; 1MMH.

    -!- SUBCELLULAR LOCATION: Integral membrane protein.
    -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97357151; PubMed=9214502; Springer M.S., Cleven G.C., Madsen O.J., de Jong W.W., 1 Amrine H.M., Stanhope M.J.; "Endemic Africa manmals shake the phylogenetic tree.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   019014;
15-JUL-1998
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Proboscidea; Elephantidae; Elephas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Elephas maximus (Indian elephant)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel.
15-JUL-1998 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5-JUL-1998 (Rel. 36, Created)
5-JUL-1998 (Rel. 36, Last sequence update)
5-OCT-2001 (Rel. 40, Last annotation updat lpha-2B adrenergic receptor (Alpha-2B adrenergic receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                    Lipoprotein;
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5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).
                           (POTENTIAL).
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ASP/GLU-RICH
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                                                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
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3 adrenoceptor)
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1.5e-77;
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 between the Swiss Institute or BIOIHLOUNG TO THE BUTOPEAN BIOINFORMATICS INSTITUTE. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for content of the statement is not removed.
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Stainboge M.J., Madsen U.U.,
Springer M.S.;
Springer M.S.;
"Highly congruent molecular support for a
of endemic African mammals.";
of endemic African mammals.";
nhvlogenet. Evol. 9:501-508(1998).
                                                                                                                                                        Madsen O.J.;
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Madsen O.J.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
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16-UCT-2001 (Rel. 40, Last sequence update)
16-UCT-2001 (Rel. 40, Last annotation update)
16-UCT-2001 (Rel. 40, Last annotation update)
11-ha-9R adrenergic receptor (Alpha-2B adrenoceptor)
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077721;
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Alpha-2B adrenergic rec
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                                                                                                        Stanhope M.J., Madsen O.J., Waddell V.G., Cleven G.C., de Jong W.W., Springer M.S., Madsen O.O.M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
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PROSITE; PS50262; G_PROTEIN_RECEP-
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SUBCELLULAR LOCATION: Integral membrane protein SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COL
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n coupled receptor; Transmembrane; Multigene
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    Last sequence update)
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    receptor (Alpha-2B adrenoceptor)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRC64;
                                                      COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                         (By
                                                                                                                                                                                                                                                                              Euteleostomi
                                                                                                                                                                                                                                                                                                                                     (Fragment).
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                                                                       similarity).
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RESULT 8
A2AB_CAVPO
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Best Local
                                                                                                                                                                                                                                                         A2AB CAVPO
Q60475;
01-NOV-1997
                              and alpha 2C adrenoceptor subtypes. Radioligand binding functional coupling to a CAMP-responsive reporter gene." Biochem. Pharmacol. 51:291-300(1996). In the CURTION: ALPHA-2 ADREMERGIC RECEPTORS MEDIATE THE CURDICED INHIBITION OF ADENYLATE CYCLASE THROUGH THE JPROTEINS.
                                                                                                 STRAIN=Hartley;
MEDLINE=96152573; PubMed=8573196;
Svensson S.P., Bailey T.J., Porte
Svensson of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
TRANSMEM
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TRANSMEM
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DOMAIN
TRANSMEM
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                                                                                                                                                                            Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                   01-NOV-1997
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00237; GFCRRHODOPSN.

PROSITE; PS00237; G PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-procein coupled receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Y15947; CAA75900.2; -. HSSP; P29274; 1MMH.
                                                                                               Svensson S.P., Bailey T.J., Porter A.C., Richn "Heterologous expression of the cloned guinea
                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                               NCBI_TaxID=10141;
                                                                                                                                                                                                              ADRA2B
                                                                                                                                                                                                                       Alpha-2B adrenergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000276; GPCR_Rhodpsn.
         SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                       108
                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                  48
                                                                                                                                                                                                                                                                                                                                                                                                                              81,
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                                                                                                                                                                                                                                                                                                                                       NSKRTPRRIKCIILTVWLIAA
                                                                                                                                                                                                                                                                                                                                                            NSKRTPRRIKCILLTVWLIAA
                                                                                                                                                                                                                                                                                                                                                                                  VATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      390
390
                                                                                                                                                                                                                                 (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26
37
63
73
96
118
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                                                                                                                                                                                                                                                                               STANDARD;
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36
62
72
72
117
140
156
378
378
291
151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.1%;
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         엉
         Integral membrane
O FAMILY 1 OF G-PRC
                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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6 (POTENTIAL).
EXTRACELLULAR (POTENTI
ASP/GLU-RICH (ACIDIC).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane; Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 81;
Pred. No.
                                                                                                                                                                                                                        (Alpha-2B
                                                                                                                                                                            Craniata; Vertebrata; Euteleosto
Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR
5 (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         779F849267F9F314 CRC64;
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                                                                                                                                                                                                                                                                               448
                                                                                                                                                                                                                                 update)
         G-PROTEIN CO
                                                                                                                                                                                                                        adrenoceptor).
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                                                                                                            Richman J.G.
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          COUPLED
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                                           CATECHOLAMINE-
E ACTION OF G
                                                                                                            Regan
                                                                                    and
           RECEPTORS
                                                                                                alpha
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a collaboration

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RRC OCC
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A2AB_MOUSE
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                                                                                                                             A2AB_MOUSE
P30545;
01-APR-1993
STRAIN=DBA/2; TISSUE=Liver;
MEDLINE=93129625; PubMed=1336396;
              SEQUENCE FROM N.A.
STRAIN=DBA/2; TISS
                                          NCBI_TaxID=10090;
                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                          Mus musculus
                                                                                              Alpha-2B adrenergic
                                                                                                         01-APR-1993
16-OCT-2001
                                                                                       ADRA2B
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LIPID
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DOMAIN
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DOMAIN
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PROSITE; PS00237; G_PROTEIN RECEP F1 1; 1.

PROSITE; PS00262; G_PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Transmembrane; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U25723; AAA67075.1; -. HSSP; P29274; 1MMH.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phosphorylation;
                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                 142 VISLPPLIYKGDOGP 156
                                                                                                                                                                                                               142 VISLPPLIYKGDQGP 156
                                                                                                                                                                                                                                     82 RTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTPRRIKCIILTVWLIAA
                                                                                                                                                                                                                                                                  82
                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                               RTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTPRRIKCIILTVWLIAA 141
                                                                                                        (Rel.
(Rel.
(Rel.
                                   (Mouse).
etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                             448 AA;
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39
50
76
86
109
131
154
169
193
371
                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                               STANDARD;
                                                                                       25, Created)
25, Last sequence update)
40, Last annotation update)
11c receptor (Alpha-2B adrenoceptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                        38
75
75
108
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130
153
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168
370
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163
309
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                                                                                                                                                                                                                                                                                                                            49597 MW;
                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                        16.8%;
                                                                                                                                                                                                                                                                               Score 75; DB; Pred. No. 2.1
                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                    ASP/GLU-RICH (ACIDIC).
IMPLICATED IN LIGAND BINDING (BY SIMILARITY).
IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 (POTENTIAL).
CYTOPLASMIC (F
                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
PALMITATE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).
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5 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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1 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
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                                                                                                                                             455 AA
                                                                                                                                                                                                                                                                           ; DB 1; uc., 40. 2.1e-54; 0;
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                                                                                                                                                                                                                                                                                                  Length 448,
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                                                                                                                                                                                                                                     141
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Matches
                    Query Match
Best Local
                                                    CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L009/7; ...
PIR; S28221; S28221.
HSSP; P29274; 1MMH.
                                                                                                  SITE
                                                                                                                                                        DISULFID
LIPID
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:87935; A
GO; GO:0004938; F
GO; GO:0001525; F
GO; GO:000165; F
                                                                                                                        SITE
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DOMAIN
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Pfam: PF00001; 7tm 1; 1.

PRINTS; PR00037; GPCRRHJODOPSN.

PROSITE; PS00237; GPCRRHJODOFSN.

PROSITE; PS00237; GPROTEIN_RECEP_F1 1; 1.

PROSITE; PS00237; GPROTEIN_RECEP_F1 2; 1.

G-protein coupled receptor; Transmem5rane; Multigene family; Phosphorylation; Lipoprotein; Palmitate.
                                                                                                                                                                                                                   DOMAIN
                  Local
                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M94583; AAA73895.1; -.
EMBL; L00979; AAA37131.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adrenergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=92378586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen W.-M., Chang A.C., Shie B.J., Chang Y.-H., Chang N.-C.A., "Molecular cloning and characterization of a mouse alpha 2C2 advenoceptor subtype gene.", Biochim. Biophys. Acta 1171:219-223 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WEDLINE=92378586; PubMed=1354956;
Chruscinski A.J., Link R.E., Daunt D.A., Bare
"Cloning and expression of the mouse homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THEM. Biophys. Res. Commun. 186:1280-1287(1992).
FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CINDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEINS
                  Similarity
                                                    455 AA;
      Conservative
                                                                          202
                                                                                                 185
                                                                                                                       181
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43
55
81
91
114
136
159
175
199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                       F:alpha2-adrenergic receptor activity; IDA. P:angiogenesis; IMP. P:MAPKKK cascade; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adra2b
                                                                                                                                                                                       113
135
158
174
198
377
401
410
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316
97
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                                                   50615
                 100.0%;
                            15.9%;
                                                   W.
      0
               Score 71;
Pred. No.
                                             (BY SIMILARITY).
V -> L (IN REF. 1).
MISSING (IN REF. 2).
, A3954AD76E0E6263 CRC64;
                                                                                                                                             ASP/GLU-RICH (ACIDIC).
IMPLICATED IN LIGAND BINDING
SIMILARITY).
                                                                                       IMPLICATED IN CATECHOL AGONIST BINDING
                                                                                                       IMPLICATED IN C
                                                                                                                                                                                       7 (POTENTIAL)
CYTOPLASMIC (
                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                         6 (POTENTIAL
                                                                                                                                                                                                                                  CYTOPLASMIC
                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
                                                                                                                                                                                                                                                                  CYTOPLASMIC (
4 (POTENTIAL)
                                                                                                                                                                                                                                                                                            2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL)

3 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                           (POTENTIAL)
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      Mismatches
                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
             DB 1; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      noved. Usage by and for (See http://www.isb-sib
                                                                                                             IN CATECHOL AGONIST BINDING
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There are no restrictions
ng as its content is in
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olog of the human alpha 2-C2
   ;
                        Length 455
 Indels
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E ACTION OF G
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0;
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RESULT 10
A2AB_DIDMA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
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Springer M.S.;
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5-JUL-1999 (Rel. 38, Last sequence update)
6-OCT-2001 (Rel. 40, Last annotation update)
Lpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE C
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                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Springer M.S., Cleven G.C., Madsen O.J., de Jong W.W., Amrine H.M., Stanhope M.J.; "Endemic African mammals shake the phylogenetic tree."; Nature 388:61-64(1997).
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Pfam; PF00001; 7tm_1; 1.
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-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COL
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Mammalia; Eutheria; Insectivora; Chrysochloridae; Amblysomus.
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nitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
FUNCTION: ALPHA-2 ADRENBEGIC RECEPTORS MEDIATE THE CATECHOLAMINE.
FUNCTION: ATTENDATION OF ADRIVLATE CYCLASE THROUGH THE ACTION OF G
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RESULT 12
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Pfam; PF00001; 7tm 1; 1.

PRINTS; PRO0237; GPCRRHODDPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

G-protein_coupled_receptor; Transmembrane; Multigene Phosphorylation; Lipoprotein; Palmitate.

NON_TER 1 1

TRANSNEM <1 25 1 (POTENTIAL).

DOMAIN 26 36 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@eisb-sib.ch).
                                                                                                                                  EMBL; Y12524; CAA73124.2; -. HSSP; P29274; 1MMH.
                                                                                                                                                                                                                                                                                                                Springer M.S., Cleven G.C., Madsen O., de Jong W.W., Waddell V.G., Amrine H.M., Stanhope M.J.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97357151; PubMed=9214502;
Springer M.S., Cleven G.C., Madsen
Amrine H.M., Stanhope M.J.;
"Endemic African mammals shake the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macroscelides proboscideus (Short-eared elephant shrew).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Macroscelidea; Macroscelididae; Macroscelides.
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16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                      REVISIONS TO 148 AND 255.
                                                                                                                                                                                                                                                                                                                                                                                                       Nature 388:61-64(1997).
[2]
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O FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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(BY SIMILARITY).
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Best Local Similarity
                                                                                                                                                  SEQUENCE OF 6-453 FROM N.A.

STRAIN-Sabra; TISSUE-Kidney,

MEDLINE=95275492; PubMed=7755946;

le Jossec M., Cloix J.F., Pecquery R., Giudicelli Y., Dausse "Differential sodium regulation between salt-sensitive and sa resistant Sabra rats is not due to any mutation in the renal 2B-adrenoesptor gene.";

2B-adrenoesptor gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LT 13
                                                                                                                                                                                                                                                                                                                  MEDLINE=90222177; PubMed=2158103;
Zeng D., Harrison J.K., D'Angelo D.D., Barber C.M., Tucker A.L.,
Lu Z., Lynch K.R.;
"Molecular characterization of a rat alpha 2B-adrenergic receptor.";
"Molecular characterization of a rat alpha 2B-adrenergic receptor.";
Proc. Natl. Acad. Sci. U.S.A. 87:3102-3106(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P193\overline{\overline{Z}8}, Q63021;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Alpha-2B adrenergic receptor (Alpha-2B adre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                            SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                           J. Hypertens. 8:177-182(1995). FUNCTION: ALPHA-2 ADRENERGIC RECINDUCED INHIBITION OF ADENYLATE
                                                                                               PROTEINS
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receptor (Alpha-2B adrenoceptor).
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Pred. No.
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Sciurognathi; Muridae; Murinae; Rattus.
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EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
                                                                                                                                                                              ery R., Giudicelli Y., Dausse J.P., between salt-sensitive and salt-to any mutation in the renal alpha
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                                                                                                         THE CATECHOLAMINE-
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EMBL outstation a collaboration

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RESULT
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Matches 63
                                                                                     A2AB PROHA
019054;
15-JUL-1998
15-JUL-1998
16-OCT-2001
                                                                                                                                                                                                                                                                                                                           CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                            PROHA
                              Procavia capensis habessinica (Abyssinian hyrax).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eu
Mammalia, Eutheria, Hyracoidea, Procaviidae, Procavia.
                                                                         15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alpha-2B adrenergic receptor (Alpha-2B adre
                                                                                                                                                                                                                                                                                                                                                                          SITE
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 SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X74400; CAA52411.1; -. PIR; A35642; A35642.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00001; 7tm_1;
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PS50262; G_PROTEIN_RECEP_F1_2; 1.
n coupled receptor; Transmembrane; Multigene family;
                                                                                                                                                                                           A.Y.
                                                                                                                                                                                                                                                AITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADILVATLIIPFSLANELLGY
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                                                                                                                                                                                                                                                                                                                                                                         185
                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                               t; Score 63; DB
t; Pred. No. 1.7
0; Mismatches
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(BY SIMILARITY).

C -> R (IN REF. 2).
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EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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IMPLICATED IN LIGAND BINDING
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BY SIMILARITY
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6 (POTENTIAL)
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                                                                                                                                 389
                                                                          update)
3 adrenoceptor) (Fragment).
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                                          Euteleostomi
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-A2AB BOVIN 077700; 15-JUL-1999 16-OCT-2001 28-FEB-2003

(Rel. (Rel. (Rel.

38, Created)
40, Last sequence up
41, Last annotation

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STANDARD;

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NATURE 388:61-64 (1997).

-!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
-!- FUNCTION: ALPHA-2 ADRENYLATE CYCLASE THROUGH THE ACTION OF G
                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G PROTEIN RECEP_F1 2; 1.

G-protein coupled receptor; Transmembrane; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Y12523; CAA73123.1;
HSSP; P29274; IMMH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Springer M.S., Cleven G.C., Madsen O.J., de Jong W.W., Waddell V.G., Amrine H.M., Stanhope M.J.;
"Endemic African mannals shake the phylogenetic tree.";
                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000276; GPCR_Rhodpsn
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION:
-!- SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97357151; PubMed=9214502;
66
                    79
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                                                                                         l Similarity
62; Conserv
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ilarity 100.0%;
Conservative
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TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                       MW;
                                                                                         0;
                                                                                                    Score 62;
Pred. No.
                                                                                                                                                                      IMPLICATED IN CATECHOL (BY SIMILARITY).
IMPLICATED IN CATECHOL
                                                                                                                                                                                                          IMPLICATED IN LIGAND BINDING SIMILARITY).
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BY SIMILARITY
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                                                                                          Mismatches
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Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).

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Query Match
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Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDILINE=98334573; PubMed=9667998;

Stanhope M.J., Madden O.J., Waddell V.G., Cleven G.C., de Jong W.W.,

Springer M.S.;

"Highly congruent molecular support for a diverse superordinal clade

of endemic African mammals.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Y15944; CAA75897.2; -. HSSP; P29274; 1MMH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00237; G_PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F12; 1.
G-protein coupled receptor; Transmembrane; Multigene family.

    -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
    -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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-i- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
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                                     79
66 YF 67
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62; Conserv
                                     YF 80
                                                                                          ITFLILFTIFGNALVILAVLTSRSLRAPONLFLVSLAAADILVATLIIPFSLANELLGYW 78
                                                                                                                                                                                                                                  392
392 AA;
                                                                                                                                                      13.9%; Score 62; llarity 100.0%; Pred. No. Conservative 0; Mismatcl
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IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).

CATECHOL AGONIST BINDING IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).
BY SIMILARITY.
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                    Pred. No. 1e-43;
Mismatches 0
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Q9GKZ5,
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-CT-2002 (TrEMBLrel. 22, Last annotation update)
01-CT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                              PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Receptor; Transmembrane.

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NON_TER 389 389

SEQUENCE 389 AA; 42631 MW; A9DC6F864487A2BE CRC6
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Madsen O., Scally M., Douady C., Kao D., DeBry R., Adkins R.,
Amrine H., Stanhope M., de Jong W., Springer M.;
"Parallel adaptive radiations in two major clades of placental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tupaia tana (Large tree shrew).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaia.
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Pfam; PF00001; 7tm_1; 1.
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43.0%; Score 192; DB 6; Lilarity 100.0%; Pred. No. 3.7e-178; Conservative 0; Mismatches 0;
                                                                                                                                                                      42631 MW; A9DC6F864487A2BE CRC64;
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Q8k1w8 bathyergus Q8cg78 chinchilla Q8k1r1 massoutiera

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Q9GL17;
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-OCT-2002 (TrEMBLrel. 22,
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Heilbronner U., van Kampen M., Isovich E., Fluegge G.;

"Thalamic alpha-2B adrenoceptors under chronic stress: persistent
upregulation in the paraventricular nucleus.";
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AY15033; AAN72456.1; -.

SEQUENCE 451 AA; 50356 MW; 3172403011F3BC60 CRC64;
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01-MAR-2003 (TrEMBLrel. 23,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Scandentia; Tupalidae; Tupaia.
                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                 Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                              Alpha adrenergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=37347;
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100.0%; Pred. No. 3.8e-176;
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                                                                                                                                                                                                                                                              Last sequence update)
Last annotation updat
B (Fragment).
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                                                                                                                     Felis.
                                                                                                                                                Euteleostomi;
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Query Match
Best Local S
Matches 184
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PROSITE; PR00237; GPCRHODOPSN.

PROSITE; PS00237; GPROTEIN RECEP_F1_1; 1.

G-protein coupled receptor; Receptor; Transmembrane.

NON_TER 1

NON_TER 387 387
                                                                                                 Nyctimene albiventer (common tube-nosed fruit bat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost.
Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;
Pteropodinae; Nyctimene.
NCBI_TaxID=48988;
                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002
01-MAR-2003
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083Q95;
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-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; AJ251174; CAC16689.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 409:610-614(2001).
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Madsen O., Scally M., Douady C., Kao D., DeBry R.,
Amrine H., Stanhope M., de Jong W., Springer M.;
"Parallel adaptive radiations in two major clades o
              NON_TER
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                                                        Pfam; PF00001; 7tm 1; 1.

PROSITE; PS00237; G PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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 SEQÜENCE
                                            G-protein
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=21819367; PubMed=11805285;
                                                                                                                                                                                                                                                                                                                                                                                 Alpha 2B adrenergic receptor
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389
389 1
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387 AA;
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(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 23, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                 (Fragment).
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 C203401584C560EE CRC64;
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Best Local Similarity 100.0%; Pred. No. 2.3e-170;
Matches 184; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                              Madsen O., Willemsen D., Ursing B.M., Arnason U., de Jong W "Molecular evolution of the alpha 2B adrenergic receptor."; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AJ505819; CAD44320.1; -.

InterPro; IPR000276; GPCRRHODDBJ.

Pfam; PP00001; 7m 1; 1.

Pfam; PP00001; 7m 1; 1.

PRINTS; PR00237; GFCRRHODDPSN.
                                                                                                                                                                                                                                                                                                                                                                                                            Hylomy8 suillus (short-tailed gymnure).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Insectivora; Erinaceidae; Hylomy
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01-MAR-2003
                                                                                                                                                                                                                                                                      PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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(TrEMBLrel. 22, Last sequence up
(TrEMBLrel. 23, Last annotation
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Q8MIDO;
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Madsen O., Willemsen D., Ursing B.M., Arnason U., de Jong Madsen O., Willemsen D., Ursing B.M., Arnason U., de Jong Molecular evolution of the alpha 2B adrenergic receptor. Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ505820; CAD44321.1; -.

EMBL; 18000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updatalpha 2B adrenergic receptor (Frammort)
ADRA2B.
                                                    SEQUENCE FROM N.A.

MEDLINB=21082081; PubMed=11214318;

Maddsen O., Scally M., Douady C., Kao
Amrine H., Stanhope M., de Jong W., S

"Parallel adaptive radiations in two
                                                                                                                                  Diceros bicornis (Black rhinoceros).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Perissodactyla; Rhinocerotidae;
                                                                                                                                                                                                                           Q9GL18;
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PRINTS; PR00237; GFCRRHODOPSN.

PROSITE; PS00237; G PROTEIN_RECEP_F1_1;

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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Mammalia; Eutheria;
-!- SUBCELLULAR
-!- SIMILARITY:
EMBL; AJ251184;
                                Nature 409:610-614(2001).
                                            mammals.";
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ilarity 100.0%;
Conservative
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(TrEMBLrel. 16, Last sequence up)
(TrEMBLrel. 22, Last annotation
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                      LOCATION:
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; Chordata; Craniata; Vertebrata;
; Pholidota; Manidae; Manis.
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O FAMILY 1
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0; Mismatches
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, Springer M.;
wo major clades
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Pfam; pro00237; GPCRRHODOPSN.
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PR00237; GPROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=21608557; PubMed=11743200;
Murphy W.J., Eizirik E., O'Brien S
Douady C.J., Teeling E., Ryder O.A
Springer M.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alpha :
ADRA2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
Alpha 2B adrenergic receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 294:2348-2351(2001).
EMBL; AJ315939; CAC87003.1; -.
INterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Resolution of the early placental phylogenetics.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tapirus terrestris (Lowland tapir) (Brazilian tapir).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Perissodactyla; Tapiridae; Tapirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8MK45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8MK45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS, PR00237; GFCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Receptor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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    139
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                                                                                                                  IAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASS
                                                            YFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTPRRIKCIILTVWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVILAVLTSRSLRAPQNLFLVSLAAADILVATLIIPFSLANELLGYWYFRRTWCEVYLAL
                                    YFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTPRRIKCIILTVWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDQGPQPRGRPQCKLNQEAWYILASSIGSFFAPCLIMILVYLRIYLIAKRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDQGPQPRGRPQCKLNQEAWYILASSIGSFFAPCLIMILVYLRIYLIAKRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTPRRIKCIILTVWLIAAVISLPPLIYK
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                                                                                                                                                                                                                                                                                        401 AA;
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388 AA;
                                                                                                                                                                                                 35.6%; Score 159; DB 6; L
llarity 100.0%; Pred. No. 5.3e-146;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                             1
401
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401
43835 MW;
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Ryder O.A., Stanhope
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Last annotation update)
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Pred. No.
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177
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                                                                                                                                                                                                      Indels
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AC Q8K4Y
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DT 01-OC
DT 01-OC
DT 01-MA
DE Alpha
GN ADRA2
COX Sciux
OC Eukar
OC Mamma
OC Sciux
OX NCBI-
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Best Local
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SEQUENCE FROM N.A.
MEDLINE-21608557; Publication of the Murphy W.J., Elzirik I Douady C.J., Teeling I Springer M.S.;
                                                                                                                                      Q8K4Y3
Q8K4Y3;
Q1-OCT-2002
01-OCT-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                        Receptor.
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NON_TER
SEQUENCE
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Q8K1U3;
01-OCT-2002
                                                                               Sciurus vulgaris (Red squirrel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                   Alpha 2B adrenergic ADRA2B.
                                                              Sciurus.
NCBI_TaxID=55149;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G PROTEIN_RECEP_F1_2;

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Huchon D., Madsen O., Sibbald M.J.J.B., Am Catzeflis F., de Jong W.W., Douzery E.J.P. "Rodent phylogeny and a timescale for the evidence from an extensive taxon sampling Mol. Biol. Evol. 0:0-0(2002).

IMBL; AJ427255; CAD20293.1; -.

InterPro; IPR000276; GPCR_Rhodpsn.
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01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marmota.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marmota monax (Woodchuck).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alpha 2B
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392 AA;
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(TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence up
(TrEMBLrel. 23, Last annotation
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                                                                                                                                                                                PRELIMINARY;
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                               PubMed=11743200;
                                                                                                                                                                                                                                                                                                                                                                                                       392
; 42811 MW;
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Rodentia;
                                                                                                                             receptor
            m m
                                                                                                                                                                                                                                                                                                                                                                         32.4%;
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22, Last sequence update)
23, Last annotation update)
septor (Fragment).
           O'Brien S.J
Ryder O.A.,
                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                         Score 145;
Pred. No.
                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vert
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                         3F75BC33DA390587 CRC64;
                                                                                                                                                                                                                                                                                                                                                                Mismatches
            .J., Madsen O., ., Stanhope M.J.
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thi; Sciuridae; Sciurinae;
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            Scally M.,
., de Jong
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           Jong
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           W.W.,
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Pfam; pF00001; 7tm_1; 1.
PRINTS; PR00237; GFCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP_F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GFCRRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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EMBL; AJ427256; CAD20294.1; -
InterPro; IPR000276; GPCR_Rhodpsn.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Aplodontidae; Aplodontia.
MCBI_TaxID=51342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Eukaryota; Metazoa; Chordata; Cran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alpha 2B adrenergic receptor (Fragment).
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Pred. No. 1.9e-129;
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PRINTS; PR00237; GPCRRHODDPSN.
PROSITE; PS00237; GPCTEIN RECEP_F1 1; 1.
PROSITE; PS00237; GPROTEIN RECEP_F1 2; 1.
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PROSITE; PS00262; GPCR RE
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01.MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation updat
Alpha adrenergic receptor 2B (Fragment).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;
Pteropodinae; Cynopterus.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
SEQUENCE FROM N.A.
                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
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Madsen O., Scally M., Douady C., Kao D., DeBry R.,
Amrine H., Stanhope M., de Jong W., Springer M.;
"Parallel adaptive radiations in two major clades
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                                                        NCBI_TaxID=9720;
                                                                                                                              Phoca vitulina (Harbor seal).
Eukaryota; Metazoa; Chordata;
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                                                                                                     Carnivora;
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TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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                                                                                           Craniata; Vertebrata; ; Pinnipedia; Phocidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145
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Best Local S
Matches 140
                                                                                                                                                                                        Huchon D., Madsen O., Sibbald M.J.J.B., Ament K., & Catzefils F., de Jong W.W., Douzery E.J.P.;
"Rodent phylogeny and a timescale for the evolution evidence from an extensive taxon sampling using the Mol. Biol. Evol. 0:0-0(2002).

EMBL; AJ427252; CAD20290.1;
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                            Receptor.
NON_TER
NON_TER
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Q8KIW8;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat.
Alpha 2B adrenergic receptor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bathyergus suillus (Cape dune mole-rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Bathyergidae;
                                                                                                     SEQUENCE
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Receptor; Tran
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-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
-!- SIMILARITY: BELLONGS TO FAMILY 1 OF G-PROTEIN COUI
EMBL; AJ251176; CAC16696.1; -...
InterPro; IPR000276; GPCR Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00037; GECRRHODOPSN.
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Madden O., Scally M., Douady C., Kao D., DeBry R., Adkins R.,
Amrine H., Stanhope M., de Jong W., Springer M.;
"Parallel adaptive radiations in two major clades of placental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139
     140;
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389 I
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389 AA;
     Conservative
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                                                                                                  389.
42728 MW;
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                    31.3%; Score 140; DB 11; 100.0%; Pred. No. 1.6e-127;
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RESULT 15
Q8CG78
ID Q8CG7
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Chinchilla lanigera.
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Huchon D., Madsen O., Sibbald M.J.J.B., Ament K., St Catzefils F., de Jong W.W., Douzery E.J.P.;

"Rodent phylogeny and a timescale for the evolution evidence from an extensive taxon sampling using thre Mol. Biol. Evol. 0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                               OBCG78,

01-MAR-2003 (TrEMBLrel. 23, Created)

01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                            SEQUENCE
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Mammalia; Eutheria;
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## ALIGNMENTS

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17-APR-2000; 2000US-0551744
                                                                                         17-APR-2001; 2001WO-US12575.
                                                                                                                                                                                                                                                                                                                                                                                                               Domain
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10-AUG-2000; 2000US-0636259. 19-OCT-2000; 2000US-0692077.

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease associated with the corresponding a polymorphic site -
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                                                                                                                            NSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGS
                                     ASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEEE
                                                       ASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGOGOKEGVCGASPEDEAEEE
                                                                          FFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALASV
                                                                                     FFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALASV
                                                                                                                                                                VATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEY
                                                                                                                                                                                                      MDHQDPYSVQATAAIAAAITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADIL
                                                                                                               NSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGS
                                                                                                                                                      VATLIIPESLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEY
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ilarity 100.0%;
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Pred. No. 7.3e-199;
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                                             The present sequence is human alpha2B-adrenoceptor (alpha2B-AR) variant protein. Alpha2B-AR has a glutamic acid repeat element (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino acids (amino acids 294-311), located in the third intracellular loop of the receptor polypeptide. The variant is obtained by deletion of three glutamates from the Glu repeat (amino acids 307-309). Alpha2B-AR gene is located on chromosome 2. Alpha2-AR mediate many of the physiological effects of the catecholamines, norepinephrine and epinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating a mammal suffering from vascular contraction of coronary arteries and a disease involving vascular contraction of coronary arteries which is clinically expressed as Prinzmetal's variant form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Snapir A, H
Scheinin M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of coronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; Page 26-27; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAD04761.
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Valkonen V;
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  Disclosure;
                                          alpha-2-adrenoceptor
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Page 26-27; 35pp;
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                                                                                                                                                                                                                                                                         Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity phosphorylation; inositol phosphate; alpha-2BAR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                           Location/Qualifiers
167.399
/note= "featured in
                                                                                                      170..193
                                                                           /label= transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
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Pred. No. 7.3e-199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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/label= polymorphic\_site
/note= "Polymorphic site

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Best Local
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10-AUG-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                              alpha2A or alpha2C or fragment or comprising a polymorphic site, comprising, b) detecting a polymediactide encoding an alpha-2B, (b) detecting a polymorphic site comprision or alpha-2B apolymorphic site comprision of a site comprision.
                                                                                                                                                                                                                                                                                                                                                     disease associated with the corresponding receptor comprises detecting a polymorphic site -
                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                      Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing
                                                                                                                                                                                                                                                                                                                                                                                                                                   (LIGG/)
(SMAL/)
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                                                                                             Similarity
                                                     MDHQDPYSVQATAAIAAAITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADIL 60
NSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGS
                        VATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEY
                                      VATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEY
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                                                                                                                   450
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; 2000US-0692077.
                                                                                      Conservative
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/label= polypmorphic_site
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                                                                                             99.5%;
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Pred. No. 7.6e-198;
0; Mismatches 0;
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                                                                                                                                                                             deletion of loop of the arteries -
                                                                                                                                                                                             New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of coronal
                                                                                                                                                                                                                                                                                                     WPI; 2001-300318/31.
N-PSDB; AAD04762.
                                                                                                                                                                                                                                                                                                                                                                                                        Snapir A,
Scheinin
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                                                                                                                                                                                                                                                                                                                                                              Heinonen P, A-Salonen JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQLTREKRFTFVLAVVIGVFVLCWFDFFFSYSLGAICPKHCKVPHGLFQFFFWIGYCNSS
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T, Tuomainen T
, Valkonen V;
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T, Lakka
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The present sequence is human alpha2B-adrenoceptor (alpha2B-AR) protein. Alpha2B-AR has a glutamic acid repeat element (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino acids (amino acids 294-311), located in the third intracellular loop of the receptor

Disclosure;

Page

29-31; 37pp;

English

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                                                                                                                                                                                                                                                                                                         Human; hypertension; alpha-2B-adrenoceptor; hypertension; hypotensive.
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by determining the pattern of alleles encoding
alpha-2-adrenoceptor -
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                                                                    AQLTREKRFTFVLAVVIGVFVLCWFFFFFSYSLGAICPKHCKVPHGLFQFFFWIGYCNSS
                                                                                                                                                             ASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEEE
                                                                                                                                                                                      ASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEA---
                                                                                                                                                                                                                                                                    NSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGS
                                                                                                                                                                                                                                                                                                                          VATLI I PFSLANELLGYWYFRRTWCEVYLALDVLFCTSSI VHLCAISLDRYWAVSRALEY
                                                                                                                                                                                                                                                                                                                                                                              MDHQDPYSVQATAAIAAAITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      450 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                              99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2351.5; DB 2: Pred. No. 7.6e-198;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                          447
 450
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a variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
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RESULT 7
ABP8170
ID ABP8
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g protein-coupled receptor; GPCR; antigenic peptide; G protein-coupled receptor modulator; antibody; immun growth related disease; cell regeneration-related disimmunological-related cell proliferative disease; aut
                                                                          Human alpha
                                                                                                        04-MAR-2003
                                                                                                                                  ABP81780;
                                                                                                                                                               ABP81780
                                                                                                                                                               standard;
                                                                         2b-adrenoceptor
                                                                                                      (first
                                                                                                                                                               Protein;
                                                                                                    entry)
                                                                       protein
                                                                                                                                                               450
                                                                         OBS
                                                                          ij
                                                                          NO:42.
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ide; gene therapy; immune-related disease; id disease; AIDS; cancer;

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The present invention describes antigenic peptides (I) comprising:

(C) (a) any one of 1601 sequences (see ABBR2019) to ABP83619) of 12-24 amino (C) (a) any one of 1601 sequences (see ABBR2019) to ABP83619) of 12-24 amino (C) (a) an isolated (1) an assay for the detection of a particular (C) and (2) an isolated antibody having high specificity and high affinity (C) are avidity for a particular GPCR. (I) can be used as GPCR modulators and (2) an isolated antibody having high specificity and high affinity (C) an antibody against a particular GPCR, and in the production of specific antibodies. The apprince of corresponding GPCRs are useful in detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell cregeneration-related diseases, growth-related dell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, procozoan or viral infections, atherosclerosis, bacterial, fungal, procozoan or viral infections, costacatthritis, osteoporossis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host (disease, parkinson's disease, multiple sclerosis, pain, psoriasis, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or ther offices are involved. The antibodies may be used in immunoassays and immunodiagnosis, ABZ42523 to ABZ4269 encode (C) epcR proteins given in ABB91675 to ABB92018, which are used in the
                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypertension; hypotension; renal disorder; rheumatoid ulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-AUG-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                              445;
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                                                                                                                        VATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEY 120
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NSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGS
                                                                              VATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEY
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98.9%;
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Pred. No. 3.8e-197;
1; Mismatches 1;
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Matches
          Query Match
Best Local (
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                                                                         Clone NGC-alpha2beta was isolated from a human spleen genomic library by screening with a fragment of the human 5-HT1A receptor gene. The gene was used to express recombinant receptor protein which can be used to produce antibodies for inhibition of receptor
                                                                                                                                                               Isolated DNA encoding human adrenergic receptor - for det
nucleic acids encoding alpha, 2-beta adrenergic receptor,
                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                Weinshank RL,
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                                                                                                                                                                                                                                                                                                                     01-OCT-1991
                                                                                                                                                                                                                                                                                                                                           US5053337-A
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                    Neurotransmission; adrenaline; epinephrine; NGC-alpha2beta.
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                                                                                                                               Disclosure; Fig 2; 15pp;
                                                                                                                                                     screening drugs.
                                           Sequence
                                                                                                                                                                                                                                                    (NEUR-) NEUROGENETIC CORP.
                                                                 function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 NSKRIPRRIKCIILIVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGS
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439;
            Similarity
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                                            487 AA
  Conservative
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            97.4%;
                                                                                                                                                                                                                                   PR;
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   2
           Score 2302.5; DB 12; Pred. No. 1.7e-193;
   Mismatches
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Human alpha-2B adrenergic receptor (AAWi1804) is a member of the rhodopsin-like signal transducer family. Its amino acid sequence was deduced from a genomic DNA clone (AAT59499) obtd. from a human spleen DNA library. Vectors have been adapted to allow prodn. of
                                                                                                                                                            Assay
cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alpha-2b adrenergic receptor; adrenoceptor; adrenaline; epinephrine; signal transduction; neurotransmitter; ligand
                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                               30-OCT-1989;
30-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW11804 standard; Protein; 487
                                                                                                                                                                                                                                                                                               Hart1g
                                                                                                                                                                                                                                                                                                                                                                                            22-OCT-1992;
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DB; AATS9499.
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91US-0707604.
92US-0965040.
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                                                                                                               2A-E;
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                                                                                                               English
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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LNPVIYTIENQDERRAFRRILCREWTQTAW
               LNPVIYTIFNQDFRRAFRRILCRPWTQTAW 447
                                                EEEEEEEECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRR
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                                                                                                 EEEEEEEECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRR
                                                                                                                                                   ASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          487 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                   97.4%;
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Pred. No. 1.7e-193;
2; Mismatches 6; I
 487
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RESULT 10
AAR48699
G-protein coupled receptor; ligand binding assay; transmembrane psychotic disorder; schizophrenia; dopamine; cAMP; adenosine; th muscarinic acetylcholine; adrenergic; endothelin; bombesin; endorhodopsin; opsin; odorant; cytomegalovirus.
                                                                                                                                                                           G-protein coupled human
                                                                                                                                                                                                                                      AAR48699
                                                                                                                                                                                               05-JUN-1996
                                                                                                                                                                                                                   AAR48699
                           10-SEP-1992;
                                              09-SEP-1993;
                                                                 17-MAR-1994
                                                                                     WO9405695-A1
         VINU ( YNYU)
                                                                                                        sapiens.
                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                               (first entry)
         NEW
                           92US-0943236.
                                               93WO-US08528
         YORK STATE
                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                            alpha-2
                                                                                                                                                                                                                                      330
                                                                                                                                                                            C2 adrenergic receptor protein
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endocrine;

thrombin;

domain;

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RESULT 11
AAW02671
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Best Local
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G-protein coupled receptor; ligand binding assay; transmembrane
                                                                 25-MAR-2003
12-NOV-1996
                                                                                                         AAW02671;
                                                                                                                                  AAW02671 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteins AAR48685-R48758 represent a range of G-protein coupled receptor proteins selected from cAMP, adenosine, muscarinic acetylcholine, adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin, odorant, cytomegaloviral and other G-protein coupled receptors. The receptor proteins were used to design polypeptides, pref. based on the binding assays. The polypeptide fragments retain biological activity such as binding a GPR ligand or modulating GPR ligand binding to a GPR such as binding a GPR ligand or modulating GPR ligand binding to a GPR compositions for treating subjects suffering from a pathology related to a GPR abnormality e.g. a psychotic disorder such as schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 72-73; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptides of G-coupled binding GPR ligands or mod
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72
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21; Conservative
                                                                                                                                                                                                                                                                   VVIGVEVLCWEPEFFSYSLGAICPKHCKVPHGLFQFEFWIGYCNSSLNPVIYTIFNQDFR
                                                                                                                                                                                                                                                                                                                       VPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFTFVLA
                                                                                                                                                                                                RMFRRILCRPWTQTAW 330
                                                                                                                                                                                                                            RAFRRILCRPWTQTAW 447
                                                                                                                                                                                                                                               VVIGVEVLĆWEPEFESYSLGAICPKHCKVPHGLFQFFFWIGYCNSSLNPVIYTIENODE-
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                                     coupled
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAAIAAAITFLILIFTIFGNALVILAVLTSRSLRAPQNLFLVSIAAADILVATLIIPFSLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             330 AA;
                                                              (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s of G-coupled receptor proteins (
                           human alpha-2 C2 adrenergic receptor.
                                                                                                                                 peptide; 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.6%;
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; Pred. No. 2.4e
6; Mismatches
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  domain;
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Matches 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Column 69-72; 184pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New dopamine receptor peptide - useful as antipsychotic for treating schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Updated on
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10-SEP-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                schizophrenia; dopamine; camp; adenosine; thrombin; adrener muscarinic acetylcholine; endothelin; bombesin; endocrine; odorant; cytomegalovirus; serotonergic.
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                 VVIGVEVLCWEPFFEFSYSLGAICPKHCKVPHGLFQFFFWIGYCNSSLNPVIYTIFNQDFR
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VVIGVFVLCWFPFFFSYSLGAICPKHCKVPHGLFQFFFWIGYCNSSLNPVIYTIFNQDF-
                                                                         VPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAQLTRBKRFTFVLA
                                                                                                                                                                                          YLRIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALASVASAREVNGHSK 251
                                                                                                                                     STGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEEEEEEEEEEEPQA
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                                                                                                                                                                    YLRIYLIAKRSNRRGPRAKCGPGQGESKQPRPDHGGAIASAKLPAIAS
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                                                                                                                                                                                                                                         IILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGSFPAPCLIMILV
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92US-0943236.
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Pred. No. 2.4e-134;
6; Mismatches 3;
                                                      GRGVGAIGGOWWRRRAHVTREKRFTFVLA
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CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic CC receptor gene (I)-(III) by detecting a polymorphic site, comprising; CC (a) obtaining a sample having a polymorphic site comprising; CC alpha2A or alpha2C or fragment or complement of; and CC (b) detecting a polymorphic site comprising mucleotide position 73 of (IIV) CC or a site comprising (ytosine or guanine at position 75 of (IIV) CC or a site comprising (A) (ggggggggg) or (B) (gggggggtgga) at CC (positions 961-972 of (III). The method may be used for genotyping an CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine CC whether an individual is at increased risk of developing a disease associated with alpha2B, alpha2A or alpha2, comprising detecting a CC polymorphic site which correlate to disease selected from cardiovascular CC disease, central nervous system disease and combinations of these. In CC addition, the technique may be used to predict an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, CC combinations of these) or antagonist (e.g. epinephrine, CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, CC ralwelscine, idazoxan, tolazoline, phentolamine and combinations of completermined response (where the response is correlated to adenyly) and CC curlates. May kinsee activity, phosphorylation or inosital phosphafe
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                                                                                                                                                                                                                                                                                                                                                                                                Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting a polymorphic site -
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predetermined cyclase, MAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-APR-2000;
10-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                 Claim 48; Page 154-155; 163pp; English
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19-OCT-2000; 2000US-0692077
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                                                       LIGGETT S B.
SMALL K M.
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53.2%;
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic CC receptor gene (I)-(III) by detecting a polymorphic site, comprising; CC (a) obtaining a sample having a polymucleotide encoding an alpha-2B, CC (a) phazA or alpha2C or fragment or complement of; and (b) detecting a polymorphic site comprising nucleotide positions 901-909 (CC of (I), a site comprising cytosine or guanine at position 753 of (IIV) (CC or a site comprising (A)) (ggggcgggcg) or (B) (ggggggggdgdg) at (CC positions 961-972 of (III). The method may be used for genotyping an alpha2B, alpha2A or alpha2C receptor gene and further used to determine (CC alpha2B, alpha2A) at increased risk of developing a disease comprising elected with alpha2B, alpha2A or alpha2, comprising detecting a glymorphic site which correlate to disease selected from cardiovascular (CC polymorphic site which correlate to disease and combinations of these. In (CC disease, central nervous system disease and combinations of these. In (CC combinations of these) or antagonist (e.g. epinephrine, prazosin, ARC 239, crauwolscine, idazoxan, tolazoline, phentolamine and combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, crauwolscine, idazoxan, tolazoline, phentolamine and combinations of these) by detecting the polymorphic site and correlated to adenylyl (cc cyclase, MAP kinase activity, phosphorylation or inositol phosphate (cc levels). The present sequence is that of the human alpha-2AAR protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease associated with the a polymorphic site -
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DB; AAI99917.
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                                                                                                      --VGAIGGQWWRRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPKHCKVPHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYSVQATAAIAAAITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADILVATLI 65
                                      LFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCR
                                                                                ERVGAAKASRWRGRQ-
                                                                                                                                                                 SDHAERPPGPRRPERGPRGKGKARASQVKPGD--SLPRRGPG----ATGIGTPAAGPGE
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Disclosure;

Fig 1;

523pp;

English

disease

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RESULT 14
ABP81779
G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; growth-related disease; growth-related disease; cell regeneration-related disease; growth-related disease; cell regeneration-related disease; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoparthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
                                                                                                                                                                                                                                                                                                                                                 New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease cancer or autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NO:40
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The present invention describes antigenic peptides (I) comprising:

(C (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino completed: (I) an assay for the detection of a particular completed: (I) an assay for the detection of a particular completed: (I) an assay for the detection of a particular completed: (I) can be used as GPCR modulators and (2) an isolated antibody having high specificity and high affinity completed: (I) can be used as GPCR modulators and completed: (I) can be used as GPCR modulators and completed: (I) can be used as GPCR modulators and completed: (I) can be used as GPCR modulators and completed: (I) can be used as GPCR modulators and completed: (I) can be used as GPCR modulators and completed: (I) can antibodies. The peptides and antibodies are also useful for detecting the complete completed: (I) can be useful for detecting the complete completed: (I) can be useful for detecting the complete completed: (I) can be useful for designing drugs for complete completed: (I) can be useful for diseases, cell completed: (I) can be useful for diseases, cell completed: (I) can be useful for diseases, completed: (I) can be useful for diseases, cell completed: (I) can be useful for diseases, can be useful for diseases, can be useful for diseases, can be useful for diseases, can be useful for complete co osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis, ABZ4253 to ABZ42869 encode GPCR proteins given in ABPB1675 to ABB82018, which are used in the ō, the present

Sequence

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ARMSULT 15
AAMS2126
ID AAMS2
XX AAS2
XX 18-FE
XX 18-FE
XX Human
XX Human
XX POlym
KW Centr
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Best Local Similarity
Matches 241; Conser
                                                                                                                                                                                                                                                                                                                                                                                        Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenlyly cyclase; MAP kinase activity phosphorylation; inositol phosphate; alpha-2CAR.
                                                     17-APR-2000; 2000US-0551744.
10-AUG-2000; 2000US-0636259.
19-OCT-2000; 2000US-0692077.
                                                                                                                              17-APR-2001; 2001WO-US12575
                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM52126 standard; Protein; 457
   (LIGG/) LIGGETT S (SMAL/) SMALL K M
                                                                                                                                                                                                       WO200179561-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alpha-2CAR variant protein.
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PRRIKAIIITCWVISAVISFPPLISIEKKGGGGGPQP-AEPRCEINDQKWYVISSCIGSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDEAEB-----EBEEEEECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGV 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPALASVASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAPCLIMILVYLRIYLIAKR-----SNRRGPRAKGGPGQGESKQPR---PDHGGALASAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPFSLANEVMGYWYFGKTWCEIYLALDVLFCTSSIVHLCAISLDRYWSITQAIEYNLKRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SASGLP--RRRAGAGGONLEKRETEVLAVVIGVEVVCWEPFFFTYTLTAV---GCSVPRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAIGGQWWRRRAQL---TREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPKHCKVPHG
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                                                                                                                                                                                                                                                                             label transmembrane_domain
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CC alpha2A or alpha2C or fragment or complement of; and CC (b) detecting a polymorphic site complement of; and CC (c) detecting a polymorphic site complement of; and CC of (I), a site comprising cytosine or guanine at positions 901-909 CC or a site comprising (A) (ggggggggcg) or (B) (ggggggggtggg) at CC opsitions 961-972 of (III). The method may be used for genotyping an CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine CC whether an individual is at increased risk of developing a disease CC associated with alpha2B, alpha2A or alpha2, comprising detecting a CC polymorphic site which correlate to disease selected from cardiovascular CC disease, central nervous system disease and combinations of these. In CC addition, the technique may be used to predict an individual's response CC norepinephrine, clonidine, oxymetazoline, guanabenz, UR14304, BHT933 and CC combinations of these) or antagonist (e.g. whimbine, prazosin, ARC 239, CT rauwolscine, idazoxan, tolazoline, phentolamine and combinations of these by detecting the polymorphic site and correlating the site to a predetermined response (where the response is correlated to adenylyl CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate CC levels). The present sequence is that of the human alpha-2CAR variant CC protein, deleted for a 4 amino acid polymorphic site at residues 321-324 of the wildtype protein (AAMS2124).
                          Query Match
                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting a polymorphic site -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to genotyping an alpha-2B, 2A, or receptor gene (I)-(III) by detecting a polymorphic site, (a) obtaining a sample having a polynucleotide encoding alpha2A or alpha2C or fragment or complement of; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 78; Page 160-162; 163pp;
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45.8%;
51.5%;
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Score 1082; DB Pred. No. 2e-86;
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an alpha-2B,
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Matches Local Similarity 235; 67 46 7 Conservative 43; Mismatches 104; Indels 74;

Gaps

밁 S 밁 S 밁 ð 밁 8 밁 ঠ 밁 S S 밁 243 221 166 106 405 183 PFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTP FQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCR 440 GVGAIGGQWWRRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFFSYSLGAICPKHCKVPHGL RRIKCIILTVWLIAAVISLPPLI--YKGDQGPQPRGR--PQCKLNQEAWYILASSIGSFF EGGAGGADGQGAAESGALTASRSPGPGGRLSRASSRSVEFFLSRRRARSSV-----KEGVCGASPEDEAEEEEEEEEECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGR PTTENGLGAAAGEAR----TGTARPRPPTWSRTRAAQRPRGGAPGPLRRGGRRRAGA AREVNGHSKSTGEKEEGETPEDTGT-RALPPSW-----AALPNSG---APCLIMGLVYARIYRVAKRTR APCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALASVAS PFSLANELMAYWYFGQVWCGVYLALDVLFCTSSIVHLCAISLDRYWSVTQAVEYNLKRTP YSAGAVAGLAAVVGFLIVFTVVGNVLVVIAVLTSRALRAPQNLFLVSLASADILVATLVM CRRKVAQAREKRETEVLAVVMGVEVLCWFPFFFIYSLYGICREACQVPGPL -----TLSEKRAPVGPDGAS S 413 404 257 242 126 66 220

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Result
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Maximum DB seq length: 2000000000
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1: /cgm2_6/ptodata/1,

2: /cgm2_6/ptodata/1,

3: /cgm2_6/ptodata/1,

4: /cgm2_6/ptodata/1,

5: /cgm2_6/ptodata/1,

6: /cgm2_6/ptodata/1,
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US-08-118-270-22
PCT-US93-08528-22
PCT-US93-08528-21
PCT-US93-08528-11
PCT-US93-08528-19
US-08-118-270-19
PCT-US93-08528-11
US-08-76-9999-11
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US-08-97-28-611-2
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US-08-78-091-29
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US-09-378-074-20 US-09-378-074-20 US-09-467-568-10 US-09-030-582-10 US-08-444-734A-7 US-08-466-855A-22 US-08-28-932-4 US-08-28-932-4 US-08-28-932-4 US-08-28-932-4 US-08-28-932-4 US-08-28-932-4 US-08-28-932-4 US-08-28-932-4 US-08-28-932-4 US-08-28-932-4 US-08-28-932-4 US-08-28-932-4 US-08-28-932-4 US-08-28-932-4 US-08-28-932-4 US-08-28-932-4 US-08-172-190-4 US-08-172-190-4 US-09-18-4-15-4 US-09-18-4-15-4 US-09-18-4-15-4 US-09-18-4-15-4

ALIGNMENTS

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PCT
                                                                                                              TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
                                                                                                                                                                                                                                                                                NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: New York University
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                        STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 YLRIYLIAKRSNRRGGPRAKGGPGQGESKQPRPDHGGALASAKLPALASVASAREVNGHSK 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 NELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTFRRIKC
                                                                                         amino acid
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              TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEEEEEEEEEEEPQA
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419 Seventh Street, N.W.,
                                                                                                                 330 amino acids
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                     linear
                                                                                                                                                                                                                                                               202-628-5197
           peptide
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Patent No. 5474898
GENERAL INFORMATION:
APPLICANT: Vencer, John C.
APPLICANT: McCombie, William R.
APPLICANT: MCCOmbie, William R.
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                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,174
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: ISTAELSEN, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH101.001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 08-FEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Newport Beach
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372 VVIGVEVLCWFPEFESYSLGAICPKHCKVPHGLFQFFFWIGYCNSSLNPVIYTTENQDFR 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFTFVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YLRIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALASVASAREVNGHSK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGSPFAPCLIMILV 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTPRRIKC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3E: Knobbe, Martens, olson and Bear
620 Newport Center Drive, Sixteenth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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Pred. No. 1.5e-107;
6; Mismatches 3;
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#YPOTHETICAL: NO
#ANTI-SENSE: NO
#FRAGMENT TYPE: internal
US-08-194-338-5
                                                                                                                                                                                                                                                                          Sequence 8, Application US/08444734A Patent No. 5610282 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                           TITLE OF INVENTION: cDNA encoding the rat D1 dopamine TITLE OF INVENTION: receptor linked to admylyl cyclase TITLE OF INVENTION: expression of the receptor protein TITLE OF INVENTION: cell lines
                                                                                                           NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                            APPLICANT:
ZIP: 92660
COMPUTER READABLE FORM:
                                                       STREET: 620 Newport CITY: Newport Beach
                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 450 amino acida
TYPE: amino acid
STRANDEDNESS: single
                                COUNTRY:
                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDEAEE-----EEEEEEECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGV 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRRIKCIILTVWLIAAVISLPPLI----YKGDQGPQPRGRPQCKLNQEAWYILASSIGSF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PYSLQVTLTLVCLAGLLMLLTVFGNVLVIIAVFTSRALKAPQNLFLVSLASADILVATLV
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                                                                             E: Knobbe, Martens, Olson and Bear
620 Newport Center Drive, Sixteenth Floor
                                USA
                                                                                                                                                                                                        Monsma, Frederick J.
Mahan, Lawrence C.
McVittie, Loris D.
                                                                                                                                                                                                                                                       Sibley, David R.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/548,714
FILING DATE: 06-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: NIH065.001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO:
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HYPOTHETICAL: N
ANTI-SENSE: NO
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APPLICATION NUMBER: US 08
FILING DATE: 03-MAR-1993
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 47.5%; Score 1122; DB 1; Local Similarity 52.7%; Pred. No. 7.5e-72; hes 241; Conservative 53; Mismatches 101;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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                  LFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCR 440
                                                              SASGLP--RRAGAGGONREKRFTFVLAVVIGVFVVCWFPFFFTYTLTAV---GCSVPRT
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                                                                                    GAIGGQWWRRRAQL---TREKRFTFVLAVVIGVFVLCWFPFFFFSYSLGAICPKHCKVPHG 403
                                                                                                                                                                                                AEPLPT----QLNG---APGEPAPA-GPRDTDALDLEES-
                                                                                                                                                                                                                                 LPALASVASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASP 293
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LFKFFFWFGYCNSSLNPVIYTIFNHDFRRAFKKILCR
                                                                                                                               SDHAERPPGPRRPERGPRGKGKARASQVKPGDSLRGAGRGRRGS-----GRRLQGRGR
                                                                                                                                                              EDEAEE-----EEEEEEECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGV 346
                                                                                                                                                                                                                                                                  FAPCLIMILVYVRIYQLAKRTRVPPSRRGPDAVAAPPGGTERRPNGLGPERSAGPGGAE
                                                                                                                                                                                                                                                                                                 FAPCLIMILVYLRIYLIAKR-----SNRRGPRAKGGPGQGESKQPR---PDHGGALASAK 233
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443
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RESULT 5 US-08-194-338-4

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Sequence 4, Application US/08194338

Patent No.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (619) 235-85;
TELEPAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US
FILING DATE: 08-FEB-15
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: pro
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: int
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Venter, John C.
APPLICANT: Fraser, Claire M.
APPLICANT: MCCOmbie, William R.
TITLE OF INVENTION: OCTOPAMINE RECEPTOR
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, olson and Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: NITELECOMMUNICATION INFORMATION: TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 620 MC. Each
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                                   285
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EGGAGGA-
                                                                                              AREVNGHSKSTGEKEEGETPEDTGT-RALPPSWAAL-----PNSG-------QGQ 284
                                                                                                                                                                  APCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALASVAS
                                                                                                                                                                                                                                     RRIKCIILTVWLIAAVISLPPLI--YKGDQGPQPRGR--PQCKLNQEAWYILASSIGSFF
                                                                                                                                                                                                                                                                                     PFSLANELMAYWYFGQVWCGVYLALDVLFCTSSIVHLCAISLDRYWSVTGAVEYNLKRTP
                                                                                                                                                                                                                                                                                                         PFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTP 126
                                                                                                                                                                                                                                                                                                                                                         YSAGAVAGLAAVVGELIVETYVGNVLVVIAVLTSRALRAPQNLFLVSLASADILVATLVM
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                                   KEGVCGASPEDEAEEEEEEEEEEEPQAVPVSPASACSPPLQQPQGSRVLATLRG-QVLLG 343
                                                                      PTTENGLGAAAGEAR - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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-DGQGAGPGAAQSGALTASRSP--GPGGRLSRASSRSVEFFLS
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                                                                      -TGTARPRPPTWARTRAAQRPRGGAPGPLRRGGRRRAGA
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No. 5508384
                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 210; Conserv
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APPLICANT: Murphy
APPLICANT: Schust
                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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Alo Seventh Street, N.W.,
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180 NHLVYVRIYQIAKRRTRVPPSRRGPDACSAPPGGADRRPNAVGPERGAGTA-------
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                                                                                                                                       72 NELLGYMYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTFRRIKC 131
                                                                                                                                                                                                            12 TAAIAAAITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADILVATLIIPFSLA 71
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                        MILVYLRIYLIAKR-----SNRRGPRAKGGPGQGESKQPR---PDHGGALASAKLPALAS
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                                                                                 IILTVWLIAAVISLPPLIY----KGDQGPQPRGRPQCKLNQRAWYILASSIGSFFAPCLI 187
                                                                                                                    NEVM-YWYFGKVWCEIYLAIDVLFCTSSIVHLCAISLDRYWSITQAIEYNLKRTPRRIKA 119
                                                                                                                                                                              TLTLVCIAGLIMLFTVEGNVLVIIAVETSRALKAPONLFLVSIASADILVATLVIPESLA 60
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                                                                                                                                                                                                                                                                                                                                                                         334 amino acids
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202-737-3528
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; pred. No. 2e-65;
46; Mismatches 59;
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                                                                                                                                                                                                                                                                     Length 334;
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/ MOLECULE TYPE:
PCT-US93-08528-22
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                                                                                                                                               Matches 210;
                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Versior
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILLING DATE: 09-SEP-193
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSEND, NUMBER: MURPHY=2 PCT
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 334 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                Local Similarity
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                                                                                        12 TAAIAAAITFLILFTIFGNALVILAVLTSRSLRAPONLFLVSLAAADILVATLIIPFSLA
   61
                    72 NELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTPRRIKC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20004
                                                                                                                                                                                                                                                                                         amino acid
NEVM-YWYFGKVWCEIYLAIDVLFCTSSIVHLCAISLDRYWSITQAIEYNLKRTPRRIKA 119
                                                                         TLTLVCIAGLIMLFTVFGNVLVIIAVFTSRALKAPQNLFLVSIASADILVATLVIPFSLA
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                                                                                                                                           43.5%; ilarity 47.6%; Conservative 4
                                                                                                                                                                                                                                                           linear
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                                                             Query Match
Best Local S
Matches 218
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Patent No. 5942414
GENERAL INFORMATION:
APPLICANT: Yi Li and Mark D. Adams
TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPETECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,971
FILING DATE: 06-UIN-1995
                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPB: Floppy disk
                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: not
                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Roseland
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27 PYSLQVTLTLVCLAGLLMLLTVFGNVLVIIAVFTSRALKAPQNLFLVXSLASADILVAXX
                  6 PYSVQATAAIAAAITFLILFTIFGNALVILAVLTSRSLRAPQNLFLV-SLAAADILVA--
                                                                            Similarity
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3E: Cecchi, Stewart & Olstein
6 Becker Farm Road
                                                                                                                                                                                                                                                        201-994-1744
                                                               Conservative
                                                                                                                                                           not relevant
                                                                                                                                           protein
                                                                                                                                                                          not relevant
                                                          43:5%; Score 1027; DB 2;
48.8%; Pred. No. 3e-65;
ative 39; Mismatches 56;
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                                                                                           Length 358;
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                                                               Gaps
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RESULT 9
US-08-118-270-21
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                                                                                TELEX: 248633
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/118,270
                                                                                                                                                       NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                            FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                               STRANDEDNESS:
                                                                                                                                       TELEFAX:
                  TOPOLOGY:
                                                    TYPE:
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Schuster, David I.
Schuster, David I.
SCHUSTER, DOLYPEPTIDES OF G-COUPLED PROTEIN
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                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                  FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
                                                                                                                                    FILING DATE: 09-SEP-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                           REFERENCE/DOCKET NUMBER: MITTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND M
                                                                                                                                                                                            COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: Patenti
                                                         REGISTRATION NUMBER:
TELEFAX:
              TELEPHONE:
                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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               202-628-5197
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                                            MURPHY=2
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Pred. No. 1.4e-63;
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                                                                                                                                                                                             Version
                                                                                                                                                                                                                                                                                                                                     Suite 300
                                                                                                                                                                                               #1.25
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RESULT 11
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Best Local Similarity
                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Schuster, David I.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 34.8
CORRESPONDENCE ADDRESS:
ADDRESSEB: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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CITY: Washington
                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                           STATE:
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                                                                                                                                                                                                                                                            419 Seventh Street,
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50.5%; Pred. No. 1.4e-63;
tive 40; Mismatches 48;
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US 07/943,236
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                                                                                                                    APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND ME
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MUJ
TELECOMMUNICATION INFORMATION:
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                                                                                         STATE: D.C.
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Local Similarity 48.6%;
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TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                         CITY: Washington
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PCT-US93-08528-19
                                                                                        Sequence 11, Application US/08196989B Patent No. 5585476 GENERAL INFORMATION:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                         APPLICANT: MacLennan, A. John
TITLE OF INVENTION: Molecular Cloning
TITLE OF INVENTION: G-Protein Coupled
               NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US93/08521
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
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TELEPAX: 202-737-3528
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CURRENT APPLICATION DATA:
    ADDRESSEE:
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STRANDEDNESS: sir
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REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2
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PatentIn Release #1.0, Version #1
Saliwanchik & Saliwanchik
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Receptors
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FILING DATE: 15-FEB-1994
CLASSIFICATION: 536
ATTORNEY/AGENTY -: 536
ATTORNEY/AGENTY -: 536
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TOPOLOGY: not
MOLECULE TYPE: |
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NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,
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CITY: G
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202; Conserv
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IYTIFNHDFRRAFKKILC
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46.1%; Pred. No. 5.4e-60;
tive 37; Mismatches 173
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; Sequence 11, Applicat ; Patent No. 5856443 ; GENERAL INFORMATION:

Application US/08760936

APPLICANT:

MacLennan,

A. John

RESULT 14 US-08-760-936-11

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NAME: PACE, DOTAN R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: MACTELECOMMUNICATION INFORMATION:
TELECHHONE: 352-375-8100
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APPLICATION NUMBER: US,
FILING DATE: December of CLASSIFICATION: 536
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: not relevant
TOPOLOGY: not relevant
LECULE TYPE: protein
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IYTIFNHDFRRAFKKILC 442
                                 IYTIFNODFRRAFRRILC 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.4%; Score 954; DB 2; Lilarity 46.1%; Pred. No. 5.4e-60; Conservative 37; Mismatches 173;
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Best Local Similarity
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FILING DATE: 04-JAN-1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,936
FILING DATE: 6-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/196,989
FILING DATE: 15-FEB-1994
ATTORNEY/AGENT IMPORMATION:
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STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: MA
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EEEEECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAQLT 361
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2421 N.W. 41st Street, Suite A-1
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46.1%; Pred. No. 5.4e-60;
Ltive 37; Mismatches 173; Indels
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Receptors
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Search completed: February 6, 2004, 18:20:53 Job time : 16.9498 secs	425 IYTIENHDERRAFKXILC 442	422 IYTIFNQDFRRAFRRILC 439	368 REKRETEVLAVVIGVEVVCWEPEFETYTLTAVGCSVERTLEKEFEWEGYCNSSLNPV 424	362 REKRPTFVLAVVIGVFVLCWFPFFFSYSLGAICPKHCKVPHGLFQFFFWIGYCNSSLNPV 421

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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seq length: 2000000000
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1: /cgn2_6/ptcodata/1/pubpaa/VCT_NEW_PUB.pep:*

2: /cgn2_6/ptcodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptcodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptcodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptcodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptcodata/1/pubpaa/US07_NEW_PUB.pep:*

7: /cgn2_6/ptcodata/1/pubpaa/US08_NEW_PUB.pep:*

9: /cgn2_6/ptcodata/1/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptcodata/1/pubpaa/US09E_PUBCOMB.pep:*

10: /cgn2_6/ptcodata/1/pubpaa/US09E_PUBCOMB.pep:*

11: /cgn2_6/ptcodata/1/pubpaa/US09E_PUBCOMB.pep:*

12: /cgn2_6/ptcodata/1/pubpaa/US09E_PUBCOMB.pep:*

13: /cgn2_6/ptcodata/1/pubpaa/US09E_PUBCOMB.pep:*

14: /cgn2_6/ptcodata/1/pubpaa/US10E_PUBCOMB.pep:*

15: /cgn2_6/ptcodata/1/pubpaa/US10E_PUBCOMB.pep:*

16: /cgn2_6/ptcodata/1/pubpaa/US10E_PUBCOMB.pep:*

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17: /cgn2_6/ptcodata/1/pubpaa/US10E_PUBCOMB.pep:*

18: /cgn2_6/ptcodata/1/pubpaa/US10E_PUB.pep:*
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2363
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                                                                                                                                                                                                                                                                                              Length
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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   15 US-10-077-870-2
15 US-10-077-870-2
15 US-10-071-073-8
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15 US-10-001-073-7
15 US-10-001-073-26
15 US-10-001-073-26
15 US-10-255-5678-40
15 US-10-255-5678-40
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                            Sequence 2, Appli
Sequence 8, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 27, Appl
Sequence 27, Appl
Sequence 26, Appl
Sequence 40, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 44, Appl
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Θ-	US-10-238-129-8	-10-054-	US-10-241-313-4	US-10-054-616A-5	US-10-054-616A-4	US-10-054-616A-2	US-10-292-798-658	US-10-225-567A-102	US-10-157-031-78	US-10-060-795B-11	US-10-352-684A-2	-238-	US-10-238-667-10	-10-238-129-1		US-10-238-667-4	US-10-238-129-4	US-10-185-991-4	US-10-052-589-2	-930-	US-09-951-622-10	0-017	0-224-26	US-10-060-795B-2	US-10-224-260-22	US-10-292-798-460	US-10-225-567A-106	US-10-336-489-8	US-09-884-430-8
œ	8	ω •	4	5	4	Sequence 2, Appli	65		78,	ä		10, App	10	e 10,	36,	4		4	Sequence 2, Appli	Į,	10, ,	75	20	е 2	e 22, 1	e 46	Sequence 106, App	ω,	Sequence 8, Appli

## ALIGNMENTS

RESULT 1 US-09-825-923-2

Sequence 2, Application US/09825923 Patent No. US20010016338A1 GENERAL INFORMATION:

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; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-923-2
                                                                                                                                                                  APPLICANT: Salonen, Riitta
APPLICANT: Kauhanen, Jussi
APPLICANT: Valkonen, Veli-Pekka
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-AR variant
CURRENT APPLICATION UMBER: US/09/825,923
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION UMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
Query Match
Best Local Similarity
Matches 447; Conserv
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Pesonen, Ullamari
Scheinin, Mika
Salonen, Jukka T
Tuomainen, Tomi-Pekka
Takka, Timo A
Nyyss'nen, Kristiina
Salonen, Riitta
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Alhopuro, Pia
Karvonen, Matti
    Conservative
                      100.0%; Score 2363; DB 9; 100.0%; Pred. No. 2.7e-166;
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    Mismatches
                                          Length 447;
  Indels
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-077-870-2
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US-10-077-870-2
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Publication No. US20030003470A1
GENERAL INFORMATION:
APPLICANT: Salonen, Jukka T
TITLE OF INVENTION: Method for detecting a risk of hypertension and
FILE REFERENCE: 0933-0183P
                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 2363; DB 15; Length Best Local Similarity 100.0%; Pred. No. 2.7e-166; Matches 447; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/077,870
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: FI 20010323
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 447
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                    FFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALASV
                                                                      NSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGS
                                                                                                                                              VATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEY
FFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGESKQPRDHGGALASAKLPALASV
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US-10-001-073-8
; Sequence 8, Application US/10001073
; Publication No. US20030113725A1
; GENERAL INFORMATION:
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APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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TYPE: PRT
ORGANISM: Homo sapiens
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447; Conserv
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                                       VIYTIFNQDFRRAFRRILCRPWTQTAW 447
                                                                                     TREKRETEVLAVVIGVEVLCWEPEFESYSLGAICPKHCKVPHGLEQFEFWIGYCNSSLNP
                                                                                                                     TREKRETEVLAVVIGVEVLCWEPEEESYSLGAICPKHCKVPHGLEQEEEWIGYCNSSLNP
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APPLICANT: Scheinin, Mika
APPLICANT: Scheinin, Mika
APPLICANT: Scheinin, Mika
APPLICANT: Tuomainen, Tomi-Pekka
APPLICANT: Lakka, Timo A
APPLICANT: Lakka, Timo A
APPLICANT: Nyyss"nen, Kristiina
APPLICANT: Kauhanen, Jussi
APPLICANT: Valkonen, Veli-Pekka
ITILE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
ITILE OF INVENTION: protein, and uses thereof:
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-923-4
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Best Local Similarity 99.3%;
Matches 447; Conservative
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APPLICANT: Heinone
APPLICANT: Alhopur
APPLICANT: Karvone
APPLICANT: Koulu,
APPLICANT: Pesonen
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Patent No. US20010016338A1
 421
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                                   LNPVIYTIFNODFRRAFRRILCRPWTQTAW 447
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Koulu, Markku
Pesonen, Ullamari
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Pred. No. 1.9e-165;
0; Mismatches 0;
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RESULT 5 US-10-077-870-4

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; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo :
US-10-001-073-7
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US-10-001-073-7
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-077-870-4
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                                                                      CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
SEQ ID NO 7
                                                                                                                                                                  Sequence 7, Application US/10001073

Publication No. US20030113725A1
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor
FILE REFERENCE: 13073-PCT
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Best Local Similarity 99.3%;
Matches 447; Conservation
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PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
SOPTWARE: Patentin Ver. 3.1
SEQ ID NO 4
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Publication No. US20030003470A1
GENERAL INFORMATION:
APPLICANT: Salonen, Jukka T
TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
FILE REFERENCE: 0933-0183P
CURRENT APPLICATION NUMBER: US/10/077,870
CURRENT FILING DATE: 2002-05-21
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Pred. No. 1.9e-165;
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APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: ROUBH, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
I PRIOR FILING DATE: 2000-12-19
SOFTMARE: Patentin version 3.1
SEQ ID NO 42
LENCTH: 450
TYPE: PRI
COGGANISM: Homo sapiens
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Best Local Similarity 98.9
Matches 445; Conservative
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Matches 447
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447; Conserv
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                                  VATLIIPPSLANBILGYWYFRRTWCBVYLALDVLFCTSSIVHLCALSLDRYWAVSRALBY
                                                                                              MDHQDÞÝSVQÁTAAÍÁAÁÍTFLÍLFTÍFGNÁLVÍLÁVLTSRSLRÁÞONLFLVSLÁAÁDÍL
                                                                                                                MDHQDFYSVQATAAIAAAITELILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADIL
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                                                                                                                                                                                99.2%;
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                                                                                                                                                                 1; Mismatches
                                                                                                                                                                           Score 2343.5; DB 15; Length Pred. No. 7.6e-165;
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APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001/073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
SEQ ID NO 27
SEQ ID NO 27
TYPE: PRT
CORRANISM: Homo sapiens
US-10-001-073-27
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US-10-001-073-27
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Best Local Similarity
Matches 243; Conserv
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Publication No. US20030113725A1
GENERAL INFORMATION:
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                                                                                                                     234 LPALASVASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGOGOKEGVCGASP 293
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                                                                                              AEPLPT----QLNG---APGEPAPA-GPRDTDALDLEES--
--VGAIGGQWWRRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPKHCKVPHG 403
                               SDHAERPPGPRRPERGPRGKGKARASQVKPGD--SLPRRGPG-----ATGIGTPAAGPGE
                                                         EDEAEE-----EEBEEEECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRG- 345
                                                                                                                                                      PAPCLIMILVYVRÍYQIÁKKRTRVÞÞSKKGÞDÁVAAÞÞGGTERRÞKGLGÞERSAGÞGGÁE 265
                                                                                                                                                                          FAPCLIMILVYLRIYLIAKR-----SNRRGPRAKGGPGQGESKQPR----PDHGGALASAK 233
                                                                                                                                                                                                                PRRIKCIILTVWLIAAVISLPPLI----YKGDQGPQPRGRPQCKLNQEAWYILASSIGSF 181
                                                                                                                                                                                                                                                                             LNPVIYTIFNQDFRRAFRRILCRPWTQTAW
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                                                                                                                                                                                                                                                                                                                                                                                                         47.7%; Score 1126; DB 15; 53.2%; Pred. No. 4.9e-75; tive 50; Mismatches 102;
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APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic recep
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 26
TENCTU. 450
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US-10-001-073-26
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; ORGANISM: Homo sapiens
US-10-001-073-26
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Sequence 40, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 47.6%; Score 1124; DB 15
Best Local Similarity 53.2%; Pred. No. 6.9e-75;
Matches 243; Conservative 49; Mismatches 103
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                                                                                                                                                                                              LPKFFFWFGYCNSSLNPVIYTIFNHDFRRAFKKILCR
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; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND AN
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PATENTIN VETSION 3.1
; SEQ ID NO 40
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-40
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                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                              Sequence 44, Application US/10225567A Publication No. US20030113798A1
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Best Local Similarity
                                                                                                                                                                                                  -10-225-567A-44
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
                                                                                                                         APPLICANT: LifeSpan Biosciences
                                                                                                                                                                                                                                                                                                              404
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                                                                                                                                                                                                                                                                                                                                                 SASGLP--RRRAGAGGQNLEKRFTFVLAVVIGVFVVCWFPFFFTYTLTAV---GCSVPRT 406
                                                                                                                                                                                                                                                                                                                                                                      GAIGGQWWRRRAQL---TREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPKHCKVPHG 403
                                                                                                                                                                                                                                                                                                                                                                                                                      SDHAERPPGPRRPERGPRGKGKARASQVKPGDSLRGAGRGRRGS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDEAEE-----EEEEEEECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGV 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRRIKATITCWVISAVISFPPLISIEKKGGGGPQP-AEPRCEINDQKWYVISSCIGSF
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52.7%;
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Pred. No. 2.3e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 102;
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                                                       PROTEIN-COUPLED
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                                                      RECEPTORS
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SOFTWARE: PatentIn version SEQ ID NO 44 LENGTH: 461 TYPE: PRT

PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292

ORGANISM: Homo -10-225-567A-44

sapiens

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Query Match
Best Local Similarity 52:5%;
Matches 240; Conservative 4

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RESULT 12 US-10-001-073-46

sequence 46, Application US/10001073 publication No. US20030113725A1

US-10-001-073-46

LENGTH: 458
TYPE: PRT
ORGANISM: Homo

sapiens

Query Match Best Local S Matches 236

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APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
APPLICANT: Small, Kirsten
APPLICANT: Small, Kirsten
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
TILE REFERENCE: 13073-PCT
FILE REFERENCE: 2001-11-01
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 46
FENCHUM: AEA
                                                                                                                                            y Match 45.4%; Score 1073.5; DB 15; Lengt Local Similarity 52.9%; Pred. No. 3.8e-71; Local Similarity 47; Mismatches 110; Indels nes 236; Conservative 47; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PESLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTF 126
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                                                             PFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTP 126
RRVKATIVAVWLISAVISFPPLVSLYR-----OPDGAAYPQCGLNDETWYILSSCIGSFF
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Pred. No. 1.3e-71;
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APPLICANT: Small, Kirsten
APPLICANT: Small, Kirsten
APPLICANT: Small, Kirsten
APPLICANT: Malpha-2-adrenergic receptor politite of invention: Alpha-2-adrenergic receptor politite of invention unumber: US/10/001,073
CURRENT APPLICATION UNUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 44
LENGTH: 462
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US-10-001-073-44
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Local Similarity 53.9%; Pred. No. 5.3e-71;
hes 241; Conservative 45; Mismatches 110;
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                                                                                                                                       AGAGE-NGHCAPPPADVEPDESSAAAERRRRR-----GALRRGGRRRAGAEGGAGGA---
                                                                                                                                                                                        WRRRAQLTREKRETEVLAVVIGVEVLCWEDEFESYSLGAICPKHCKVPHGLEQEFEWIGY 413
                                                                                      -----DGQGAGPGÅAESGALTÅSRSP--GPGGRLSRÅSSRSVEFFLSRRRARSSVC 368
                                                                                                             DEAEEEEEEEECEPQAVPVSPASACSPPLQQPQGSRVLATLRG-QVLLGRGVGAIGGQW 353
                                    CNSSLNPVIYTIFNQDFRRAFRRILCR
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CNSSLNPVIYTVFNQDFRPSFKHILFR 454

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Sequence 4, Application US/10060795B
Publication No. US20030040022A1
GENERAL INFORMATION:
APPLICANT: Civelli Olivier
APPLICANT: Bunzow, James R.
APPLICANT: Bunzow, James R.
APPLICANT: Grandy, David K.
APPLICANT: Machida, Curtis A.
TITLE OF INVENTION: Dopamine Receptors and Ge-
FILE REFERENCE: 90-1992-CCC
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CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: 09/238977
PRIOR TILING DATE: 1999-01-27
PRIOR PELICATION NUMBER: 08/474892
PRIOR PELICATION NUMBER: 08/474892
PRIOR FILING DATE: 1995-06-07
PRIOR PELICATION NUMBER: 07/97358
PRIOR PELICATION NUMBER: 07/97358
PRIOR APPLICATION NUMBER: 07/43854
PRIOR APPLICATION NUMBER: 07/43854
PRIOR PILING DATE: 1989-11-20
PRIOR PELICATION NUMBER: 07/273373
PRIOR PELICATION NUMBER: 07/273373
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ORGANISM: Homo sapiens
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                                           IYTIFNQDFRRAFRRILCR 440
                                                                                                           REKRETEVLAVVIGMEVVCWEPEEETYTLTAV---GCSVPRTLEKEEPWPGYCNSSLNPV
IYTLENHDERRAFWKILCR 306
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CURRENT FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: PCT/US00/02125
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 09/448,076
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: 09/276,400
PRIOR APPLICATION NUMBER: 09/276,400
PRIOR FILING DATE: 1999-03-25
PRIOR FILING DATE: 1999-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Ver
SEQ ID NO 84
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                       Matches 167;
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PRIOR FILING DATE: 1998-03-27
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PRIOR FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: 09/014,195
PRIOR FILING DATE: 1998-01-27
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PRIOR APPLICATION NUMBER: 09/561,381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 601
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FILING DATE: 1998-01-27
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293 FVATRRIRERARANKLNTÍÁLKSTELEÞMÁNSSÝVAASNSGSKSRLLASWLCCGRDRAQ 352
                                                                                                                      136 VWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGSFFAPCLIMILVYLRI 195
                                                                                                                                                                                                                                                      113 ALVLSVIIVLTIIGNILVILSVFTYKPLRIVQNFFIVSLAVADLTVALLVLPFNVAYSIL
                                                                                                                                                                                                                                                                          76 GYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTPRRIKCIILT 135
                                                                                                                                                                  GRWEFGIHLCKLWLTCDVLCCTSSILNLCAIALDRYWAITDPINYAQKRTVGRVLLLISG
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                                       - IAKRSNRRGPRAKGGPG---
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Listing first 45 summaries
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2363
1 MDHQDPYSVQATAAIAAAIT.....QDFRRAFRRILCRPWTQTAW 447
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Copyright (c) 1993 - 2004 Compugen Ltd.
SUMMARIES
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<b>4</b> 5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
557	564	567	567	570	573	574.5	575	576	578	578	579	580	580	580	581
23.6	23.9	24.0	24.0	24.1	24.2	24.3	24.3	24.4	24.5	24.5	24.5	24.5	24.5	24.5	24.6
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A53279	T18863	JH0447	T16079	139369	S68423	A47174	B30341	JC1525	D56849	I38209	A38731	S08146	DYMSD2	DYHUD4	DYXLD2
serotonin receptor	hypothetical prote	alpha-1A-adrenergi	hypothetical prote	alpha-1A-adrenergi	serotonin receptor	serotonin receptor	G protein-coupled	alpha-1B-adrenergi	dopamine receptor-	serotonin receptor	alpha-1A adrenergi	dopamine receptor	dopamine receptor	dopamine receptor	dopamine receptor

## ALIGNMENTS

A;Map position: 2p13-2q13 C;Superfamily: vertebrate rhodopsin C;Superfamily: vertebrate rhodopsin C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein Query Match 99.2%; Score 2343.5; DB 2; Length 450; Best Local Similarity 98.9%; Pred. No. 1.1e-154; Matches 445; Conservative 1; Mismatches 1; Indels 3; Gaps 1;	Biochem. Biophys. Res. Commun. 172, 817-823, 1990 A;Title: In vitro amplification by polymerase chain reaction of a partial gene encoding (A;Reference number: A36158; MUID:91054503; PMID:2173582 A;Accession: A36158 A;Molecule type: DNA A;Residues: 95-361, 'QL', 364-389 < CHA> A;Cross-references: GB:M38742; NID:9177867; PIDN:AAA62823.1; PID:9177868 C;Genetics: A;Gene: GDB:ADRA2B; ADRARL1; ADRA2L1; ADRA2RL1 A;Cross-references: GDB:120539; OMIM:104260	A; Residues: 1-450 - CLOMS A; Cross-references: GB:M34041; NID:g178197; PIDN:AAA51666.1; PID:g178198 A; Cross-references: GB:M34041; NID:g178197; PIDN:AAA51666.1; PID:g178198 A; Cross-references: GB:M34041; NID:g178197; PIDN:AAA51666.1; PID:g178198 A; Cross-references: GB:A41244, 1991 A; Title: Identification of an additional gene belonging to the alpha(2) adrenergic recept A; Title: Identification of an additional gene belonging to the alpha(2) adrenergic recept A; Title: Identification of an additional gene belonging to the alpha(2) adrenergic recept A; Title: Identification of an additional gene belonging to the alpha(2) adrenergic recept A; Title: Identification of an additional gene belonging to the alpha(2) adrenergic recept A; Title: Identification of an additional gene belonging to the alpha(2) adrenergic recept A; Title: Identification of an additional gene belonging to the alpha(2) adrenergic recept A; Title: Identification of an additional gene belonging to the alpha(2) adrenergic recept A; Title: Identification of an additional gene belonging to the alpha(2) adrenergic recept A; Title: Identification of an additional gene belonging to the alpha(2) adrenergic recept A; Title: Identification of an additional gene belonging to the alpha(2) adrenergic recept A; Title: Identification of an additional gene belonging to the alpha(2) adrenergic recept A; Title: Identification of an additional gene belonging to the alpha(2) adrenergic recept A; Title: Identification of an additional gene belonging to the alpha(2) adrenergic recept A; Title: Identification of an additional gene belonging to the alpha(2) adrenergic recept A; Title: Identification of an additional gene belonging to the alpha(2) adrenergic recept A; Title: Identification of an additional gene belonging to the alpha(2) adrenergic recept A; Title: Identification of an additional gene belonging to the alpha(2) adrenergic recept A; Title: Identification of an additional gene belonging to the alpha(2) adrenergic recept A; Title: Identification of an	R;Weinshank, R.L.; Zgombick, J.M.; Macchi, M.; Adham, N.; Lichtblau, H.; Branchek, T.A.; Mol. Pharmacol. 38, 681-688, 1990 A;Title: Cloning, expression, and pharmacological characterization of a human alpha-28-a; A;Reference number: A37223; MUID:91042469; PMID:2172775 A;Accession: A37223 A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: DNA A;Residues: 1-450 <wei> R;Lommaney, J.W.; Lorenz, W.; Allen, L.F.; King, K.; Regan, J.W.; Yang-Feng, T.L.; Caron Proc. Natl. Acad. Sci. U.S.A. 87, 5094-5098, 1990 A;Title: Expansion of the alpha 2-adrenergic receptor family: cloning and characterizatic A;Reference number: I39407; MUID:90311349; PMID:2164221 A;Accession: I39407 A;Status: preliminary A;Molecule type: DNA</wei>	ALIGNMENTS  man nergic receptor ision 22-Jan-1993 #text_change 29-Oct-1999 08; A36158

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A;Molecule type: DNA
A;Residues: 1-448 <RES>
A;Cross-references: EMBL:X74400; NID:g840862; PIDN:CAA52411.1;
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor
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Best Local (
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                                                       FFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALAS-
                                                                                                                             NSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGS
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VASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEE
                                  FFAPCLIMILVYLRIYVIAKRSHCRGLGAXRGSGEGESKKPQPVAGGVPTSAKVPTLVSP
                                                                                                        NSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQRPEPRGLPQCELNQEAWYILASSIGS
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84.2%; Pred. No. 1.7e-130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Zeng, D.; Harrison, J.K.; D'Angelo, D.D.; Barber, C.M.; Tucker, A.L.; Lu, Proc. Natl. Acad. Sci. U.S.A. 87, 3102-3106, 1990
A;Title: Molecular characterization of a rat alpha-2B-adrenergic receptor.
A;Reference number: A35642; MUID:90222177; PMID:2158103
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A1964-2B-adrenergic receptor - rat
alpha-2B-attus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
RESULT
S28221
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A; Residues: 1-453 <ZEN>
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77; Conservative
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                                                                                                                                                                                                                   | SEEVEECEPQTLPASPASVCNPPLQQPQTSRVLATLRGQVLLGKNVGVASGQWWRRRTQ
                                                                                                                                                                                                                                      EEEEEEECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAQ
                                                                                                                                                                                                                                                                                                                        VASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEE
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                                                                       PVIYTVFNQDFRRAFRRILCRPWTQTGW
                                                                                                   PVIYTIFNQDFRRAFRRILCRPWTQTAW
                                                                                                                                                                   LTREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPKHCKVPHGLFQFFFWIGYCNSSLN 419
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                                                                                                                                             LSREKRFTFVLAVVIGVFVVCWFPFFFSYSLGAICPQHCKVPHGLFQFFFWIGYCNSSLN
                                                                                                                                                                                                                                                                                     LSSVGEANGHPKPPREKEEGETPEDPEARALPPTWSALPRSGQGQKKGTSGATAEEGDEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 1985.5; DB 2;
; Pred. No. 6.2e-130;
24; Mismatches 46;
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A; Molecule type: DNA
A; Residues: 6-228,231-455 < CHR>
A; Residues: 6-228,231-455 < CHR>
A; Cross-references: GB:L00979; NID:g191547; PIDN:AAA37131.1; PID
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; transmembrane protein
F;18-43/Domain: transmembrane #status predicted < TM1>
F;55-81/Domain: transmembrane #status predicted < TM3>
F;90-115/Domain: transmembrane #status predicted < TM4>
F;134-158/Domain: transmembrane #status predicted < TM5>
F;134-159/Domain: transmembrane #status predicted < TM6>
F;377-402/Domain: transmembrane #status predicted < TM6>
F;410-435/Domain: transmembrane #status predicted < TM7>
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A;Molecule type: DNA
A;Residues: 1-455 <CHE>
A;Rotesidues: 1-455 <CHE>
A;Cross-references: EMBL:M94583
A;Cross-references: EMBL:M94583
A;Rote: the authors translated the codon CCA for residue 161 as Phe, ACT for R;Chruscinski, A.J.; Link, R.E.; Daunt, D.A.; Barsh, G.S.; Kobilka, B.K.
Biochem. Biophys. Res. Commun. 186, 1280-1287, 1992
A;Title: Cloning and expression of the mouse homolog of the human alpha2-C2
A;Reference number: JH0693; MUID:92378586; PMID:1354956
A;Accession: JH0693
                                          RESULT 5
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A;Title: Molecular cloning and characterization of a mouse alpha(2)C2 A;Reference number: S28221; MUID:93129625; PMID:1336396
A;Accession: S28221
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C;Species: Mus musculus (house mouse)
C;Species: Nov-1993 #sequence_revision 26-May-1995 #text_change 13-Aug-1999
alpha 2-adrenergic re
C;Species: Rattus sp.
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Similarity 83.6%; Pred. No. 1.4e-127;
                                                                                                                                                           LNPVIYTIFNQDFRRAFRRILCRPWTQTAW 447
                                                                                                                                                                                                                   FAPCLIMILYYLRIYVIAKRSHCRGLGAKRGSGEGESKKPRPGPAAGGVPASAKVPTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FFAPCLIMILVYLRIYLIAKRSNRRGGPRAKGGPGQGESKQPRPD--HGGALASAKLPALA 238
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R;Lanier, S.M.; Downing, S.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Duzic, a.; Aller, S.M.; Aller, S.M.; Duzic, a.; Aller, S.M.; Aller, S.M.; Aller, S.M.; Aller, S.M.; Aller, S.M.; Aller, S.M.; Aller, S.M.; Aller, S.M.; Aller, S.M.; Aller, S.M.; Aller, S.M.; Aller, S.M.; Aller, S.M.; Aller, S.
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A;Residues: 1-450 <LAN>
A;Residues: 1-450 <LAN>
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A;Residues: 1-450 <LANS
A;Residues: 1-450 <LANS
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Dec-1991 #sequence_revision 03-Apr-1992 #text_change
C;Accession: B40392
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A;Molecule type: mENA
A;Residues: 1-276 <RES>
A;Cross references: GB:S67316; NID:
C;Superfamily: vertebrate rhodopsin
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                                                           PRRIKCIILTVWLIAAVISLPPLI---YKGDQGPQPRGRPQCKLNQEAWYILASSIGSFP 182
                                                                                                         PRRIKAIIVTVWVISAVISFPPLISIEKKGAGGGQQPAEPSCKINDQKWYVISSSIGSFF
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Pred. No. 1e-71;
il; Mismatches 94;
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alpha-2 adrenergic receptor - mouse
c;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
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Mol. Pharmacol. 42, 16-27, 1992

A;Title: Cloning of two moles encoding alpha-2 adrenergic receptor subtypes and in antagonist binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                APCLIMILVYLRIYLIAKR-----SNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPAL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRRIKATIVTVWVISAVISFPPLISIEKKGAGGGQQPAEPSCKINDQKWYVISSSIGSFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRRIKCIILTVWLIAAVISLPPLI---YKGDQGPQPRGRPQCKLNQEAWYILASSIGSFF
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ICPKHCKVPHGLFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCR 440
                                                                                                                                                                                                                                                                                                                                                                                                         APCLIMILVYVRIYQIAKRRTRVPPSRRGPDACSAPPGGADRRP-
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                                                                                                                                                                                                                                                                                     NGLG-----PERGAGP--TGAEAEP-----LPTQLNGAPGEPAPAGPRDGD
                                                                                                              -RGVGAIGGQWWRRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYSLGA 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.0%; Score 1135; I
52.4%; Pred. No. 3.66
tive 41; Mismatches
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3.6e-71;
hes 98;
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A; Molecule type: DNA
A; Residues: 1-103,'T',105-156,'C',158-367,'L',369-450 < KOB>
A; Residues: 1-103,'T',105-156,'C',158-367,'L',369-450 < KOB>
A; Cross-references: GB: M18415; NID: g178191; PIDN: AAA51664.1; PID: g178192
A; Note: the authors translated the codon TGT for residue 157 as Val, and A; Note: part of this sequence was confixmed by protein sequencing
A; Chhajlani, V.; Rangel, N.; Uhlen, S.; Wikberg, J.E.S.
FEBS Lett. 280, 241-244, 1991
A; Title: Identification of an additional gene belonging to the alpha(2); A; Title: Identification of an additional gene belonging to the alpha(2);
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N;Alternate names: alpha-2C10-adrenergic receptor
C;Species: Homo sapiens (man)
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A;Accession: $14311
A.Moloculo Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita Levilorita L
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A; Introns: #status absent
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A;Cross-references: GDB:120538; OMIM:104210
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Science 238, 650-656, 1987
A;Title: Cloning, sequencing, and expression of the gene A;Reference number: A40132; MUID:88042789; PMID:2823383
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C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change
C;Accession: A34169; A40132; S14311
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A; Residues: 77-123, 'P', 125-209 < CHH>
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                          SDHAERPPGPRRPERGPRGKGKARASQVKPGDSLRGAGRGRRGS-
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                                                                                                                                                                                              LPALASVASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASP
                                                                                                                                                                                                                                                                                                             FAPCLIMILVYLRIYLIAKR-----SNRRGPRAKGGPGQGESKQPR---PDHGGALASAK 233
                                                                                                                                                                                                                                                                                                                                                                                                                              PRRIKCIILTVWLIAAVISLPPLI----YKGDQGPQPRGRPQCKLNQEAWYILASSIGSF
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53.0%; Prec
52;
                                                                             EEEEEEECEPOAVPVSPASACSPPLOOPOGSRVLATLRGOVLLGRGV 346
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Pred. No. 2
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Yang-Feng, T.L.;
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2.1e-70;
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Francke, U.;
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62;

Gaps

GRRLQGRGR

351

SS

298

293

205 181 146 125 86

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RESULT 10
150829
150829
alpha 2-adrenoceptor - cuckoo wrasse
C;Species: Labrus ossifagus (cuckoo wrasse)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 13-Aug-1999
C;Accession: I50829
R;Svensson, S.P.; Bailey, T.J.; Pepperl, D.J.; Grundstrom, N.; Ala-Uotila, S.Br. J. Pharmacol. 110, 54-60, 1993
A;Title: Cloning and expression of a fish a2-adrenoceptor.
A;Reference number: I50829; MUID:94035926; PMID:7693288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
A38316
alpha-2-adrenergic receptor - pig
alpha-2-adrenergic receptor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: A38316
R;Guyer, C.A.; Horstman, D.A.; Wilson, A.L.; Clark, J.D.; Cragoe Jr., J. Biol. Chem. 265, 17307-17317, 1990
A;Title: Cloning, sequencing, and expression of the gene encoding the A;Reference number: A38316; MUID:91009167; PMID:2170371
A;Accession: A38316
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C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane
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A; Residues: 1-450 <GUY>
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F;34-59/Domain: hydrophobic <HII>
F;71-96/Domain: hydrophobic <HII>
F;10-91/JOmain: hydrophobic <III>
F;106-131/Domain: hydrophobic <IIIV
F;150-175/Domain: hydrophobic <HIV>
F;153-218/Domain: hydrophobic <HVIV
F;375-400/Domain: hydrophobic <HVIV
F;405-430/Domain: hydrophobic <VIII>
                                                                                                                                                                                                                                                                                                                                                                   alpha-2-adrenergic receptor - rat
C;Species: Rattus norvegicus (Norway ra
C;Date: 31-Dec-1991 #sequence_revision
C;Accession: JH0190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: I50829
A;Status: preliminary; translated f:
A;Status: preliminary; translated f:
A;Molecule type: DNA
A;Residues: 1-432 <SVE>
A;Cross-references: EMBL:U07743; NII
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                        A;Experimental source: brain
C;Comment: Alpha-2-adrenergic receptor is
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; tr
                                                                                                                                                                                                                                                                                              R;Chalberg, S.C.; Duda, T.; Rhine, J.A.; Sharma, R.K. Mol. Cell. Biochem. 97, 161-172, 1990
A;Title: Molecular cloning, sequencing and expression o A;Reference number: JH0190; MUID:91125329; PMID:2177834
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                                                                                                                                                                                                                                                             A; Molecule type: mRNA
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||:||:|||:|||:||| ||:|| || ||:|| 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFSLANELMGYWYFGKVWCGIYLALDVLFCTSSIVHLCAISLDRYWSVTQAVEYNLKRTP
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46.2%;
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 Score 1091;
Pred. No. 4e
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Pred. No. 7.8e-69;
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                  DB 2;
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Local Similarity hes 238; Conserv

Conservative

Mismatches

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A40392
alpha-2-adrenergic receptor (clone RG10) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Aate: 06-Dec:-1991 #sequence_revision 03-Apr-1992 #text_chang
C;Accession: A40392
R;Lanier, S.M.; Downing, S.; Duzic, E.; Homcy, C.J.
J. Biol. Chem. 266, 10470-10478, 1991
A;Title: Isolation of rat genomic clones encoding subtypes of A;Reference number: A40392; MUID:91244823; PMID:1645350
A;Accession: A40392; AUID:91244823; PMID:1645350
A;Accession: A40392
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                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-458 <LAN>
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      LPALASVASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASP
                                          CLIMGLVYARIYRVAKLRTRT-LSEKRGPARPDGASPTTENGLGKAAGENGHCAPPRTEV
                                                                                                 ŔŔVKATĪVAVWLĪSĀVĪSFPPLVSFYR---RPDGAAYPQCGLNDETWYILSSCIGSFFAP
                                                                                                                    RRIKCIILTVWLIAAVISLPPLI--YKGDQGPQPRGRPQCKLNQEAWYILASSIGSFFAP
                                                                PFSLANELMAYWYFGQVWCGVYLALDVLFCTSSIVHLCAISLDRYWSVTQAVEYNLKRTP
                                                                                                                                                                            PFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTP
                                                                                                                                                                                                                  YŚAGAVAGLAAVVGFLIVFTVVĠNVLVVIAVLTŚRALRAPQNLFLVŚLASADILVATLVM
                                                                                                                                                                                                                                           YSVQATAAIAAAITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADILVATLII
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                                                                                                                                                                                                                                                                             45.9%; Score 1084.5;
52.9%; Pred. No. 1.1e-
tive 46; Mismatches
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A;Residues: 1-458 <RES>
A;Cross-references: GB:M99376; NID:g191880;
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alpha-2 adrenergic receptor - mouse
C.Species: Mus musculus (house mouse)
C.Pate: 02-7ul-1996 #sequence_revision 02-Jul-1996 #text_change
C.Accession: I49480
R.Link, R.; Daunt, D.; Barsh, G.S.; Chruscinski, A.; Kobilka, B.
Mol. Pharmacol 42, 16-27, 1992
A.Title: Cloning of two mouse genes encoding alpha-2 adrenergic in antagonist binding.
A.Reference number: I49480; MUID:92342131; PMID:1353249
A.Recession: I49480
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39; Conservative
                                                                       FFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCR
                                                                                                                        AIGGQWWRRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPKHCKVPHGLFQF
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                                                   FFWIGYCNSSLNPVIYTVFNQDFRRSFKHILFR
                                                                                                         ARSSVCRRKVAQ-AREKRFTFVLAVVMGVFVLCWFPFFFSYSLYGICREACQLPEPLFKF
                                                                                                                                                                                          CGASPEDEAEEEEEEEEECEPQAVPVSPASACSPPLQQPQGSRVLATLRG-QVLLGRGVG
                                                                                                                                                                                                                         PRTEVEPDESSAAERRRRGALRRGGRRREG-AEGDTGS-----ADGPGPGLAAEQGA
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alpha-2C-adrenergic receptor - human (Species: Homo sapiens (man) (Species: Homo sapiens (man) (C)Species: Homo sapiens (man) (C)Species: Almar-1990 #sequence revision 31-Mar-1990 #sequence revision 31-Mar-1990 #sequence revision Alpha-1990 #sequence revision Alpha-1990 #sequence revision Alpha-1990 #sequence revision Alpha-1990 #sequence revision Alpha-1990 #sequence revision Alpha-1990 #sequence revision Alpha-1990 #sequence receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptable receptabl
FEBS Lett. 280, ....
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N;Alternate names: alpha 2C4 isoceptor
C;Species: Mus musculus (house mouse)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C;Accession: A48392
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Biochem. Mol. Biol. Inc. 29, 467-474, 1997
A;Title: Wolecular characterization of a murine homologue of alpha 2C4 adrenoceptor subt
A;Reference number: A48392; MUID:93250567; PMID:8387367
                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-461 < REG>
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A; Residues: 1-458 < CHA>
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                                              k;Chhajlani, v.,
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                Cross-references: GB:J03853; NID:g178193; PIDN:AAA35513.1;
;Chhajlani, V.; Rangel, N.; Uhlen, S.; Wikberg, J.E.S.
3BS Lett. 280, 241-244, 1991
;Title: Identification of an additional gene belonging to th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGKAAGENGHCAPPRTEVEPDESSAAERRRRR-----AAVRRGGR-RREGAEG-----
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ilarity 51.6%;
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Pred. No. 2.2e-67
47; Mismatches 9
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                       the alpha(2) adrenergic
                                                                                                                     PID:g178194
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A;Reference number: S14308; MUID:91192139; PMID:1849485
A;Accession: S14309
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 95-223 <CHH>
A;Accession: S14310
A;Molecule type: DNA
A;Residues: 95-223 <CH2>
C;Genetics:
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C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled recept
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Best Local :
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nes 240; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G protein-coupled receptor; transmembrane
                    LFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCR 440
                                                                                                                                                                                                                                                                                                                                                                                                                                      PFSLANELMAYWYFGQVWCGVYLALDVLFCTSSIVHLCAISLDRYWSVTQAVEYNLKRTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YSAGAVAGLAAVVGFLIVETYVGNVLVVIAVLTSRALRAPQNLFLVSLASADILVATLVM
LEKEFFWIGYCNSSLNPVIYTVFNQDFRPSFKHILFR
                                                                       RRRARSSVCRRKVAQ-AREKRFTFVLAVVMGVFVLCWFPFFFIYSLYGICREACQVPGP 416
                                                                                           RGVGAIGGQWWRRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPKHCKVPHG 403
                                                                                                                                               EGGAGGA---
                                                                                                                                                                               KEGVCGASPEDEAEEEEEEEEEEPQAVPVSPASACSPPLQQPQGSRVLATLRG-QVLLG 343
                                                                                                                                                                                                                   PTTENGLGAAAGEAR-----TGTARPRPPTWSRTRAAQRPRGGAPGPLRRGGRRRAGA 310
                                                                                                                                                                                                                                                                                            APCLIMGLVYARIYRVAKRRTR---
                                                                                                                                                                                                                                                                                                                         APCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALASVAS
                                                                                                                                                                                                                                                                                                                                                                 RRVKATIVAVWLISAVISFPPLVSLYR-----OPDGAAYPQCGLNDETWYILSSCIGSFF
                                                                                                                                                                                                                                                                                                                                                                                                RRIKCIILTVWLIAAVISLPPLI--YKGDQGPQPRGR--PQCKLNQEAWYILASSIGSFF 182
                                                                                                                                                                                                                                                    AREVNGHSKSTGEKEEGETPEDTGT-RALPPSW-----AALPNSG-------QGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADRA2L2; ADRA2RL2
                                                                                                                                              -DGQGAGPGAAQSGALTASRSP--GPGGRLSRASSRSVEFFLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1080; DB 2;
Pred. No. 2.4e-67;
 453
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                                                                                                                                              357
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Search completed: February 6, 2004, 18:20:09 Job time : 17.4448 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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P-OCTOPAMINE. FOR ANTAGONISTS, THE RANK ORDER IS YOHIMBINE

PHENTOLAMINE > MIANSERINE > SPIPERONE > PRAZOSIN

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SEQUENCE
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MIM; 104260; -
GO; GO:0005887; C:integr
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EMBL; M38742; AAA62823.1; -.
EMBL; AF316895; AAK01635.1; -.
EMBL; AF005900; AAB62558.1; -.
PIR; A37223; A37223.
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  61
                                                                                                                                             Similarity
                                                            MDHQDEYSVQATAAIAAAITFLILETIFGNALVILAVLTSRSLRAPQNLFLVSLAAADIL
  VATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEY 120
                                           MDHQDPYSVQATAAIAAAITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADIL
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49953 MW;
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Pred. No. 2.5e-
0; Mismatches
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IMPLICATED IN LIGAND BINDING
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01-NOV-1997
16-OCT-2001
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PRINTS; PR00237; GFCREHODDSN.

PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein_coupled_receptor; Transmembrane; Multigene Phosphorylation; Lipoprotein; Palmitate.
                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaborative between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                    modified and this statement is not remove
entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Hartley;
MEDLINE=96152573; PubMed=8573196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alpha-2B adrenergic receptor
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                                                                                            EMBL; U25723; AAA67075.1;
HSSP; P29274; 1MMH.
                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                               nterPro; IPR000276; GPCR_Rhodpsn
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(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
renergic receptor (Alpha-2B adrenoceptor).
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Hystricognathi; Caviidae; Cavia.
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EXTRACELLULAR (POTENTIAL)
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Eukaryota; Metazoa; Mammalia; Eutheria;

Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

SEQUENCE FROM N.A.

CYTOPLASMIC 2 (POTENTIAL

(POTENTIAL).

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-A2AB RAT STANDARD; PRT; 453 AA.
P19378; Q63021;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor).
ADRA2B.
Rattus norvegicus (Rat)
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(BY SIMILARITY).
8384F8757E404777 CRC64;
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Lu Z., Lynch K.R.;
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"Differential sodium regulation between salt-sensitive and salt-
resistant Sabra rate is not due to any mutation in the renal alpha
2B-adrenoceptor gene.";
Am. J. Hypertens. 8:177-182(1995).
-i- FUNCTION: ALPHA-2 ADRENGEGIC RECEPTORS MEDIATE THE CATECHOLAMII
-i- FUNCTION: ALPHA-2 ADRENGIC RECEPTORS MEDIATE THE ACTION OF ORDER OF ADENYLATE CYCLASE THROUGH THE ACTION OF ORDER OF ADENYLATE CYCLASE THROUGH THE ACTION OF ORDER OF ADENYLATE CYCLASE THROUGH THE ACTION OF ORDER OF ADENYLATE CYCLASE THROUGH THE ACTION OF ORDER OF ADENYLATE CYCLASE THROUGH THE ACTION OF ORDER OF ADENYLATE CYCLASE THROUGH THE ACTION OF ORDER OF ADENYLATE CYCLASE THROUGH THE ACTION OF ORDER OF ADENYLATE CYCLASE THROUGH THE ACTION OF ORDER OF ADENYLATE CYCLASE THROUGH THE ACTION OF ORDER OF ADENYLATE CYCLASE THROUGH THE ACTION OF ORDER OF ADENYLATE CYCLASE THROUGH THE ACTION OF ORDER OF ADENYLATE CYCLASE THROUGH THE ACTION OF ORDER OF ADENYLATE CYCLASE THROUGH THE ACTION OF ORDER OF ADENYLATE CYCLASE THROUGH THE ACTION OF ORDER OF ADENYLATE CYCLASE THROUGH THE ACTION OF ORDER OF ADENYLATE CYCLASE THROUGH THE ACTION OF ORDER OF ADENYLATE CYCLASE THROUGH THE ACTION OF ORDER OF ADENYLATE CYCLASE THROUGH THE ACTION OF ORDER OF ADENYLATE CYCLASE THROUGH THE ACTION OF ORDER OF ADENYLATE CYCLASE THROUGH THE ACTION OF ORDER OF ADENYLATE CYCLASE THROUGH THE ACTION OF ORDER OF ADENYLATE CYCLASE THROUGH THE ACTION OF ORDER OF ADENYLATE CYCLASE THROUGH THE ACTION OF ORDER OF ADENYLATE CYCLASE THROUGH THE ACTION OF ORDER OF ADENYLATE CYCLASE THROUGH THE ACTION OF ORDER OF ADENYLATE CYCLASE THROUGH THE ACTION OF ORDER OF ADENYLATE CYCLASE THROUGH THE ACTION OF ORDER OF ADENYLATE CYCLASE THROUGH THE ACTION OF ORDER OF ADENYLATE ORDER OF ADENYLATE ORDER OF ADENYLATE ORDER OF ADENYLATE ORDER OF ADENYLATE ORDER ORDER ORDER ORDER ORDER ORDER ORDER ORDER ORDER ORDER ORDER ORDER ORDER ORDER ORDER ORDER ORDER ORDER ORDER ORDER ORDER ORDER ORDER ORDER ORDER ORDER ORDER ORDER ORDER ORDER ORDER ORDE
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PROSITE; PS00237; G-PROTEIN RECEP F1_2; 1.
PROSITE; PS50262; G-PROTEIN RECEP F1_2; 1.
G-protein coupled receptor; Transmembrane; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M32061; AAA40635.1; -.
EMBL; X74400; CAA52411.1; -.
PIR; A35642; A35642.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Sabra; TISSUE=Kidney; MEDLINE=95275492; PubMed=7755946;
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SIMILARITY: BELONGS TO
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BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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J.K., D'Angelo
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PALMITATE (POTENTIAL).

ASP/GLU-RICH (ACIDIC).

IMPLICATED IN LIGAND BINDING
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87:3102-3106(1990).
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                  BCA040FFF9A310EB CRC64;
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                                                                           adrenergic receptor.",
Biochem. Biophys. Res. Commun. 186;1280-1287(1992).
-!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CINDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE
                                  This
                        between
                                                                                                                   SEQUENCE FROM N.A.

MEDILINE=92378586; PubMed=1354956;

Chruscinski A.J., Link R.E., Daunt D.A., Barsh G.S., Kobilka B.F.

"Cloning and expression of the mouse homolog of the human alpha
                                                                                                                                                                                                                                                                                                                                               P30545;
01-APR-1993
01-APR-1993
16-OCT-2001
                                                                                                                                                                              MEDLINE=93129625; PubMed=1336396; Chen W.-M., Chang A.C., Shie B.J., Chang Y.-H., Cha "Molecular cloning and characterization of a mouse adrenoceptor subtype gene."; Biochim. Blophys. Acta 1171:219-223(1992).
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MEDLINE=93129625;
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STRAIN=DBA/2; TISSUE=Liver;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                           01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor).
                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                             SUBCELLULAR LOCATION: Integral membrane SIMILARITY: BELONGS TO FAMILY 1 OF G-PRO
                  SWISS-PROT entry is copyright.
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                                                                                                                                                                                                                                                                                                                                                                                             MOUSE
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                                                                                                                                                                                                                                                                                      Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.0%;
                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24;
                Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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Pred. No. 5.1e-109;
P4; Mismatches 46;
      It is produced through a collaboration informatics and the EMBL outstation
                                          brane protein.
G-PROTEIN COUPLED RECEPTORS
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use alpha 2C2
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E ACTION OF G
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                   collaboration
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GO; GO:0001525; E
GO; GO:0000165; E
InterPro; IPR000;
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DOMAIN
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EMBL; L00979; AAA37131.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
               246
                                    239
                                                           186
                                                                               181
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                                                                                                                                                                                                                                       376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; S28221; S
P; P29274;
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ŚPLSŚVGĖANĆHPKPPRĖKĖĖGĖTPĖDPEARĀLPPNWSĀLPRŠVODOKKGTSGĀTAĖKGĀ
               S-VASAREVNGHSKSTGEKBEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEA
                                                       FFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGESKQPRPD--HGGALASAKLPALA
                                                                                                                                                                                                                                               Similarity
                                            NSKRTPRRIKCI
                                                                                                     NSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGS
                                                                                                                                               VÁTL I I ÞÉSLANBLÍGYMY FWRANCEVYLALDVÍ FCTSSÍ VHÍCA Í SIÐR YMAVSRÁLBY
                                                                                                                                                                             MVHQEPYSVQATAAIASAITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADIL
                                                                                                                                                                                            455 AA;
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P:MAPKKK cascade;
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230 N
50615 MW;
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                                                                                                                                                                                                                                             82.6%;
83.6%;
                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                      IMPLICATED IN CATECHOL AGON
(BY SIMILARITY),
V -> L (IN REF. 1).
MISSING (IN REF. 2).
M; A3954AD76E0E6263 CRC64;
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                                                                                                                                                                                                                            Score 1951.5; DB 1; Length Pred. No. 4.8e-107; 2; Mismatches 49; Indels
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IMPLICATED IN LIGAND BINDING
SIMILARITY).
IMPLICATED IN CATECHOL AGONIS
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                    PALMITATE (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).
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5 (POTENTIAL)
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2 (POTENTIAL)
EXTRACELLULAR (POTENTIAL)
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4 (POTENTIAL
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IN CATECHOL AGONIST BINDING

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AGONIST

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Gaps

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185 180 125 (POTENTIAL)

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or send a
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A2AB_RABIT STANDARD; PRT; 394 AA
O77830;
15-JUL-1999 (Rel. 38, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                              TRANSMEM DOMAIN
                                                                                                                                                                                                     InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR000237; GFCRRHODPSN.
PROSITE; PS00237; G PROTEIN RECEP_F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                          EMBL; Y16189; CAA76115.1;
EMBL; Y15946; CAA75899.2;
HSSP; P29274; 1MMH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stanhope M.J., Madsen O.J., Waddell V.G., Clev
Springer M.S., Madsen O.O.M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ
-!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9986;
                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alpha-2B
                                                                                                                                                                                                                                                                                                                                                        s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                           PROTEINS.
SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS I
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                                                                                                                                                                                                                                                                                                                         non-profit institutions as long as its content is d and tris statement is not removed. Usage by and fo s requires a license agreement (See http://www.isb-sib.an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adrenergic
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42906
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 ¥.
                   CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).

4 (POTENTIAL).

4 (POTENTIAL).

5 (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

6 (POTENTIAL).

7 (POTENTIAL).

8 YSIMILARITY.

BY SIMILARITY.

ASP/GLU-RICH (ACIDIC).
 5D520975ACA6916A CRC64;
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B adrenoceptor)
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15-JUL-1998
28-FEB-2003
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019032;
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=97357151; PubMed=9214502;
Springer M.S., Cleven G.C., Madse
Amrine H.M., Stanhope M.J.;
"Endemic African mammals shake th
PRINTS; PR00237; GPCKRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                      EMBL; Y12522; CAA73122.2; ALT SEQ. InterPro; IPR000276; GPCR_Rhodpsn. Pfam; PF00001; 7tm_1; 1.
                                                                                       use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (see or send an email to license@isb-sib.ch).
                                                                                                                                       This SWISS-PROT entry is copyright. It is produced throug between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no res
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                     Nature 388:61-64(1997).
                                                                                                                                                                                                                                                                                                                                                                               Orycteropus
                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9818;
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                                                                                                                                                                                         SUBCELLULAR SIMILARITY:
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(Rel. 36, Last sequence upda
(Rel. 41, Last annotation up
receptor (Alpha-2B
                                                                                                                                                                                                                                                                                                                                                                                afer (Aardvark).
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                                                                                                                                                                                                     LOCATION:
                                                                                                                                                                                         BELONGS
                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Tubulidentata; Orycteropodidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.9%;
                                                                                                                                                                                                                             ADRENERGIC RECEPTORS NO OF ADENYLATE CYCLASE
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                                                                                                                                                                                         Integral membrane protein.

OF FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                        Madsen O.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1794;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                  the
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                                                                                                                                                                                                                                                                 phylogenetic
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on update)
.-2B adrenoceptor) (Fragment).
                                                                                                                                                               It is produced through
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                                                                                                                                                                                                                                                                                          de Jong
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                                                                                                               here are no restrictions as its content is in longer by and for contents.
                                                                                                                                                                                                                             MEDIATE 1
                                                                                                    http://www.isb-sib.
                                                                                                                                                                                                                                                                  tree.";
                                                                                                                                                                                                                                                                                          W. W.
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                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
Orycteropus.
                                                                                                                                                                                                                             CATECHOLAMINE-
E ACTION OF G
                                                                                                                                                                                                                                                                                           Waddell V.G.,
                                                                                                                                                   EMBL outstation
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                                                                                                                                                       collaboration
                                                                                                       ch/announce/
                                                                                                                   commercia.
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RESULT 7

A2AB ERIEU

ID A2AB ERIEU

STANDARD; PRT; 391 AA.

AC 019012;

DT 15-UUL-1998 (Rel. 36, Created)
DT 15-UUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DT A1pha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Fragment).

GN ADDRA2B.

OS Erinaceus europaeus (Western European hedgehog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalla; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.

OX NCBI_TaxID=9365;
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Matches 345
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345; Conserv
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                                                                                                                                                                                                   VÍGVEVLCWEPEFFSYSLGAÍCÞORCKVÞHGLE 388
                                                                                                                                                                                                                  VIGVFVLCWEPFFFFSYSLGAICPKHCKVPHGLF 405
                                                                                                                                                                                                                                              PASSÁSACNPPLÓOPÓGSRVLATLRGOVLLGRGLGAAGGOWWRRAQLTREKRFTFVLAV
                                                                                                                                                                                                                                                           | PVSPASACSPPLOOPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFTFVLAV
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                                                                                                                                                                                                                                                                                                                                                        RIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPAL-ASVASAREVNGHSKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                      LLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTPRXIKCII
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388 AA;
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87.8%;
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EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

FOPTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
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Pred. No. 6
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IMPLICATED IN CATECHOL AGONIST BINDING
(BY SIMILARITY).

IMPLICATED IN CATECHOL AGONIST BINDING
(BY SIMILARITY).
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ASP/GLU-RICH (ACIDIC)
IMPLICATED IN LIGAND
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EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
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2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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DOMAIN
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Pfam; PF00001; 7tm_1; 1.
PRINTS; PR0037; GPCRRHODDPSN.
PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Multigene family; Phosphorylation; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                        NIAMO
                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstati the European Bioinformatics Institute. There are no restrictions on modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 388:61-64(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Springer M.S., Cleven G.C., Madsen O.J., de Jong W.W., Amrine H.M., Stanbope M.J., "Endemic African manals shake the phylogenetic tree.";
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SEQUENCE FROM N.A.
MEDLINE=97357151; PubMed=9214502;
                        194
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SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
                                                                                              13
                                                                                                                     74
                                                                                                                                                14 AIAAAITELILETIFGNALVILAVLTSRSLRAPQNLELVSLAAADILVATUIIPESLANE
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RIYLIAKRSNRRGPRAKGGPGQESKQPRPDHGGALASAKLPALAS-VASAREVNGHSKS
                                                                                                                                                                                                    Similarity
                                                                                                 LLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALBYNSKRTPRRIKCII 133
                                     LTVWLÍAAVÍŠLÞELÍÝKGDÓSÞÓÞRGRÞÓCKLNÓBAWÝÍLASSÍGSÞÞÁÞCLÍMÍLVÝL
                                                     LTVWLIAAVISLPPLIYKGDQGPQRGBPQCKLNQEAWYILASSIGSFFAPCLIMILVYL
                                                                                                                                 AIAAVITELILETIEGNALVILAVLTSRSLRAPONLELVSLAAADILVATLIIPESLANE
                                                                                          LLGYWYFRRTWCEVYLALDVLFCTSSIVHI
                                                                                                                                                                                                                                        391 AA;
                                                                                                                                                                                         Conservative
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141
157
181
356
380
389
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37
63
73
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36
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72
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117
140
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                                                                                                                                                                                                         75.0%;
                                                                                                                                                                                                                                     42919 MW;
                                                                                                                                                                                                    88.0%;
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                                                                                                                                                                                     14;
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O FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
                                                                                                                                                                                                Score 1772.5;
Pred. No. 1.16
                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
ASP/GLU-RICH (ACIDIC).
IMPLICATED IN LIGAND BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
                                                                                                                                                                                                                                                      IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (POTENTIAL)
CYTOPLASMIC (1
2 (POTENTIAL)
                                                                                                                                                                                                                                                                                                         SIMILARITY)
                                                                                                                                                                                                                               F21FA2757B1EE1DA CRC64;
                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                   LCAISLDRYWAVSRALEYNSKRTPRRIKCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                .1e-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
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                                                                                                                                                                                                      DB 1; Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
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E THROUGH THE ACTION OF G
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5 문 Ş В Ś 밁 S 밁 Ş 밁 Ś 밁 Ś

120

60

180 193

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RESULT 8
A2AB_HORSE
ID A2AB HORSE
AC 077721;
DT 16-OCT-2001
DT 16-OCT-2001
DT 16-OCT-2001
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CC Mammallia; Edward
RA ADRAZB.
OS Equus caball
CC Mammallia; Edward
RA Springer M.
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HSSP; P29274; 1MMH.
InterPro; IPR000276; GPCR_Rhodpsn
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Madsen O.J.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CINDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=98334573; PubMed=9667998;
Stanhope M.J., Madsen O.J., Waddell V.G.,
Springer M.S.;
"Highly congruent molecular support for a
of endemic African mammals.";
Mol. Phylogenet. Evol. 9:501-508(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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16-OCT-2001 (Rel. 40, Last annotation update)
Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor)
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-i- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE
                                                                                                                                                                                                                                                 Elephas maximus (Indian elephant).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Proboscidea; Elephantidae; Elephas
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                                   SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
                                                                                    FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS I INDUCED INHIBITION OF ADENYLATE CYCLASE
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PS50262; G_PROTEIN_RECEP_F1_2; 1.
n_coupled_receptor; Transmembrane; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                     PVSPASACSPPLOOPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFTFVLAV
                                                                                                                                                          PGEKER-ETPEDPGTLTLPPSWPVLPNSGQGQKEGVCGASP-
       VIGVFVLCWFPFFFSYSLGAICPOHCKVPHGLF
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Pred. No. 2
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IMPLICATED IN CATECHOL (BY SIMILARITY)
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IMPLICATED IN LIGAND BINDING
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15-JUL-1998 (Rel. 36, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor)
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Mammalia; Eutheria; Insectivora; Chrysochloridae;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Springer M.S., Cleven G.C., Madsen O.J., de Jong W.W., Amrine H.M., Stanhope M.J.; "Endemic African mammals shake the phylogenetic tree.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97357151; PubMed=9214502;
Springer M.S., Cleven G.C., Madse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
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PROSITE; PRO0237; G PROTEIN RECEP F1 2; 1.

PROSITE; PS00237; G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Transmembrane; Multigene family;
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HSSP; P29274; 1MMH.
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nitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CEUNCTION: ALPHA-2 ADRENYLATE CYCLASE THROUGH THE INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE
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RESULT 11
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Best Local :
                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
EMBL; Y15944; CAA75897.2; -.
HSSP; P29274; 1MMH.
InterPro; 1PR000276; GPCR_Rhodpsn
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                             "Highly congruent molecular support for a diverse superordinal clade of endemic African mammals.";

Mol. Phylogenet. Evol. 9:501-508(1998).

-1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINB=98334573; PubMed=9667998;
Stanhope M.J., Madden O.J., Waddell V.G.,
Springer M.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A2AB_BOVIN
077700;
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                                                                                                                                                                   entities requires a license agreement
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28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral membrane protein (By similarity) SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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                                                                                                                                        an email to license@isb-sib.ch).
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RESULT 12
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OS DUGONG
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OC Mammal

Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor)

(Rel. 38, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation updat

Dugong dugon (Dugong). Eukaryota; Metazoa; Ch

Eutheria; Sirenia; Dugongidae;

Chordata;

Craniata; Vertebrata;

Euteleostomi

(Fragment).

Dugong

077713; 15-JUL-1999 16-OCT-2001 28-FEB-2003

A2AB DUGDU

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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Multigene family.

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VVIGVEVLCWEPPEFSYSLGAICPKHCKVPHGLF 405
                                                  VPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFTFVLA
                                                                                              STGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEEEEEEEEECEPQA
                                                                                                                                  RIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALAS-VASAREVNGHSK-
                                                                                                                                                                        LTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGSFFAPCLIMILVYL
                                                                                                                                                                                                             LLGYWYERRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTPRRIKCII
                                                                                                                                                                                                                                                    AIAAAITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAADILVATLIIPFSLANB
                                                                             RPGEKGDGETPEAPGTPALPPSWPAIPKSGQGQKEGVCGSSPEEEA--EEEEEEGCEPQA
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                                        LPASPASACSPPLQQPQGSRVLATLRGQVLLGRGTGTAGAQWWRRRTQLSREKRFTFVLA
                                                                                                                     RIYLIAKRSHCRGPRAKGGPGERESKQPHPVPGEVSDSAKLPTLASQLATPGEANGCSQP
                                                                                                                                                           LIVWLIAAVISLPPLIYKGDQGPQPLARPQCKLNQEAWYILASSIGSFFAPCLIMILVYL
                                                                                                                                                                                                    LLGYWYFWRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTPRRIKFII
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BY SIMILARITY.
POLY-GLU.
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IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
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PRINTS; PR00237; GFCRRHODOPSN.
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PS50262; G_PROTEIN_RECEP_
                                                                                                                                                                                               RIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALA-SVASAREVNGHSKS
                                                                                                                                                                                                                                                                                                                                                                                                                     AIAAAITFLILFTIFGNALVILAVLTSRSLRAÞQNLFLVSLAAADILVATLIIÞFSLANE
                                                                                                                   TGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEEEEEEEEECEPQAV
                                                                                                                                                            RIYLIAKRSHRRGPGAKGGPRKGESKQPHSLDSGPSALANLPTLASSLAVAGEANGHSMP
                                                                                                                                                                                                                                                               LTVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGSFFAPCLIMILVYL
                                                                                                                                                                                                                                                                                                                      LLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTPRRIKCII
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                    PVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFTFVLAV
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86.5%;
                                                                                  PTLPPSWPVLPNSGQGQKGGVCGASLEEEA--DKEEEECGPPAV
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_RECEP_F1_2; 1.
_Transmembrane; Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1741;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                extracellular (potential) asp/glu-rich (acidic).
BY SIMILARITY.
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PROSITE; PS50262; G_PROTEIN RECEP F1_2; 1.
G-protein coupled receptor; Transmembrane; Multigene
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PRINTS; PR00237; GPCRHJODOPSN.
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(Rel. 36, Last sequence update)
(Rel. 40, Last annotation update)
renergic receptor (Alpha-2B adrenoceptor)
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G_PROTEIN_RECEP_F1_1; 1.
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O FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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Pred. No. 6.1e-94; 
L6; Mismatches 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          de Jong W.W.,
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019025; 15-JUL-1998 16-OCT-2001 16-OCT-2001 Alpha-2B adr

998 (Rel. 36, Created)
001 (Rel. 40, Last sequence upd
001 (Rel. 40, Last annotation u
adrenergic receptor (Alpha-2B

update)
on update)
-2B adrenoceptor) (Fragment).

MACPR

A2AB\_MACPR

STANDARD;

387 AA

Macroscelides proboscideus (Short-eared elephant shrew). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Macroscelidea; Macroscelididae; Mácroscelides

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W G-protein coupled receptor; Transmembrane; Multigene family;

W Phosphorylation; Lipoprotein; Palmitate.

T NON TER

I 1 25 1 (POTENTIAL).

TOMANIN 26 36 CYTOPLASMIC (POTENTIAL).

TOMANIN 63 72 EXTRACELLULAR (POTENTIAL).

TOMANIN 73 95 3 (POTENTIAL).

TOMANIN 96 117 CYTOPLASMIC (POTENTIAL).

TOMANIN 96 117 CYTOPLASMIC (POTENTIAL).

TOMANIN 118 140 4 (POTENTIAL).

TOMANIN 118 140 4 (POTENTIAL).

TOMANIN 157 180 EXTRACELLULAR (POTENTIAL).

TOMANIN 158 159 EXTRACELLULAR (POTENTIAL).

TOMANIN 159 5 (POTENTIAL).

TOMANIN 151 156 EXTRACELLULAR (POTENTIAL).

TOMANIN 151 353 CYTOPLASMIC (POTENTIAL).

TOMANIN 151 353 CYTOPLASMIC (POTENTIAL).

TOMANIN 151 353 CYTOPLASMIC (POTENTIAL).

TOMANIN 151 353 CYTOPLASMIC (POTENTIAL).
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Best Local
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VIGVFVLCWFPFFFSYSLGAICPQHCKVPHGLF
            VIGVFVLCWFPFFFFSYSLGAICPKHCKVPHGLF
                                            RIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALA-SVASAREVNGHSKS
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                                                                                           TGEKER-ETSEDPGTPTLQRSWPVLPSSGQSQKKGVCGASPEEBAEGEEEGS---RPLSV
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86.5%;
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Pred. No. 6.9e-94;
9; Mismatches 39;
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IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).

IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
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BY SIMILARITY
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Best Local Similarity
Matches 335; Conserv
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MEDLINE=97357151; PubMed=9214502;
MEDLINE=97357151; PubMed=9214502;
Springer M.S., Cleven G.C., Madsen O.J., de Jong W.W., Waddell V.G.,
Amrine H.M., Stanhope M.J.;
"Endemic African mammals shake the phylogenetic tree.";
Nature 388:61-64(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Springer M.S., Cleven G.C., Madsen O., de Jong W.W., Waddell V.G., Amrine H.M., Stamhope M.J.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
FUNCTION: ALTERA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
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PRINTS; PR00237; GFENTEIN RECEP F1 1; 1.

PROSITE; PS00237; G-PROTEIN RECEP-F1-2; 1.

PROSITE; PS50262; G-PROTEIN RECEP-F1-2; 1.

Prostein coupled receptor; Transmembrane; Multigene family; Phosphorylation; Lipoprotein; Palmitate, NON TER 1 1 (POTENTIAL).

TRANSMEM <1 25 CYPOPLASMIT (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=29082;
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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387 1
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85.0%;
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                                                                                                Score 1697.5;
Pred. No. 2.6e:
L3; Mismatches
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2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                          7 (POTENTIAL).
ASP/GLU-RICH (ACIDIC).
BY SIMILARITY.
                                                                                                                                                                                                                                                                             6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                             4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                     (BY SIMILARITY).

IMPLICATED IN CATECHOL AGONIST BINDING (BY SIMILARITY).
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                                                                                          PTGER---ETPEDLVSPASPPSWPAIPNSGQGRKEGVCGTSPEEEA----BEEEECGPEA
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Search completed: February 6, 2004, 18:18:04 Job time : 10.9666 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1: sp_archea:*
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9: sp_plant:*
11: sp_rodent:
12: sp_virus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

16	15	14	13	12	11	10	9	8	7	6	<sub>U</sub>	4	w	N	1	Result No.
1812.5	1818.5	1820.5	1826	1829.5	1833.5	1838.5	1842.5	1843.5	1844.5	1866.5	1868.5	1956.5	1961.5	2003.5	2120	Score
76.7	77.0	77.0	77.3	77.4	77.6	77.8	78.0	78.0	78.1	79.0	79.1	82.8	83.0	84.8	89.7	Query Match Length DB
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Q925E4;
Q1-DEC-2001
Q1-DEC-2001
Q1-MAR-2003
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene promoter.";

Submitted (WAR-2001) to the EMBL/GenBank/DDBJ databases.

Submitted (WAR-2001) to the EMBL/GenBank/DDBJ databases.

INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

INTEGRAL MEMBRANE PROTEIN COUPLED RECEPTORS.

EMBL, AF366899; AAK53388.1;

INTEGRACO.276; GPCR_Rhodpsn.

INTEGRACO.276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; GPCRRHODOPSN.

PROSITE; PS00237; GPCRHODOPSN.

G-PROSITE; PS00237; GPCRHODOPSN.

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Schaak S., Cussac D., Paris H.;
"Cloning and characterization of the rat alpha2B-adrenergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Pred. No. 4.7e-
25; Mismatches
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Sciurognathi; Muridae; Murinae; Rat
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Matches 376
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Q925K7;
01-DEC-2001
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Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILAR -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN COUPLED RECEPT SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN COUPLED RECEPT SUBMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPT
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01-MAR-2003
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MGD; MGI.87935; Adražb.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
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Mammalia; Eutheria;
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PROSITE; PS50262; G PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Receptor; Transmembrane.

SEQUENCE 448 AA; 50018 MW; 1B5ED9456C0B2B73 CRC64;
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                                                                                                                                                                                                                  VATLIIPFSLANELLGYWYFWRAWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALBY
                                                                                                                                                                        VATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEY
                                                                                                                                                                                                       MVHQEPYSVQATAATASATTELTLETTI EGNALVILAVLTSRSLRAPQNLELVSLAAADTL
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)1 (TrEMBLrel. 19, I
)3 (TrEMBLrel. 23, I
)3 (receptor alpha 2B.
EBEEEEECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRRAQ
                                ŃŚKRTPRRIKCIILTWILIAAVISLPPLIYKGDORPEPHGLPOCELNOBAWYILASSIGS
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Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 1.1e
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Q925K6;
Q1-DEC-2001
Q1-DEC-2001
Q1-MAR-2003
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                DESEVEECEPOTLPASPASVFNPPLOOPQTSRVLATLRGQVLLSKNVGVASGQWWRRRTQ
                                                   LSSVGEANGHPKPPREKEEGETPEDPEARALPPNWSALPRSVQDQKKGTSGATAEKGAEE
                                                                   VASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEE
                                                                                           FFAPCLIMILVYLRIYVIAKRSHCRGLGAKRGSGEGESKKPHPAAGGVPASAKVPTLVSP
                                                                                                     FFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALAS-
                                                                                                                                                                  VATLIIPFSLANELLGYWYFWRAWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEY
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                             EEEEEEECEPQAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAQ
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1 (TrEMBLrel. 19, Last sequence update)
3 (TrEMBLrel. 23, Last annotation update)
receptor alpha 2B.
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Pred. No. 2.7e-148;
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Q8MK45;
01-OCT-2002
01-OCT-2002
01-MAR-2003
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NON_TER
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SEQUENCE
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MEDLINE=21608557; PubMed=11743200;
Murphy W.J., Bizirik E., O'Brien S.J., Madsen
Douady C.J., Teeling E., Ryder O.A., Stanhope
Springer M.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tapirus terrestris (Lowland tapir) (Brazilian tapir).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Mammalia; Eutheria; Perissodactyla; Tapiridae; Tapirus
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PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1;

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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InterPro; IPR000276; GPCR_Rhodpsn.
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Science 294:2348-2351(2001).
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Treceptor (Fragment).
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MEDLINE-21082081; PubMed=11214318;

Madsen O., Scally M., Douady C., Kao D., DeBry R.,

Marine H., Stanhope M., de Jong W., Springer M.;

"parallel adaptive radiations in two major clades"
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Nyctticebus coucang (Slow loris).
Nyctticebus coucang (Clow loris).
Eukaryota, Metazoa, Chordata, Cr
Mammalia, Eutheria, Primates, St
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Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1 1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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-i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED EMBL; AJ251186; CAC16695.1; -.
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  Q9GL07
Q9GL07;
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(TrEMBLrel. 22, Last annotation update)
argic receptor 2B (Fragment).
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Pred. No. 3.6e
11; Mismatches
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Strepsirhini; Loridae; Nycticebus.
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PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1.

RECEP_F1_2; 1.

WG-protein coupled receptor; Receptor; Transmen 1 1

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SEQUENCE 389 389
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MEDLINE=21082081; PubMed=11214318;
Madsen O., Scally M., Douady C., Kao D., De
Amrine H., Stanhope M., de Jong W., Springe
"Parallel adaptive radiations in two major
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Phoca.
                                                                                    Q9GL06;
Q9GL06;
01-MAR-2001
01-MAR-2001
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                                          Alpha adrenergic AAR2B.
    Eukaryota;
                       Sus scrofa
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    (Pig).
Metazoa;
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                                                                   (TrEMBLrel 16, Created)
(TrEMBLrel 16, Last sequence update)
(TrEMBLrel 22, Last annotation updat
irgic receptor 2B (Fragment).
                                                                                                                                                                                 PRELIMINARY;
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90.8%;
       Chordata;
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Pred. No. 2e-
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         Craniata;
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W., Springer M.;
two major clades
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Best Local S
Matches 356
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Q9GL17;
01-MAR-2001
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01-OCT-2002
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NON TER
SEQUENCE
SEQUENCE FROM N.A. MEDLINE=21082081; Madsen O., Scally
                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9685;
                                                                                                              AAR2B.
Felis silvestris
                                                                                                                                                   01-OCT-2002 (Trew Alpha adrenergic
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G_protein_coupled_receptor; Receptor; Tran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21082081; PubMed=11214318;
Madsen O., Scally M., Douady C., Kao
Amrine H., Stanhope M., de Jong W., S
"Parallel adaptive radiations in two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN
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0001; 7tm_1; 1.
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391 /
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(TTEMBLrel. 16, Last sequence up
(TTEMBLrel. 22, Last annotation
srgic receptor 2B (Fragment).
                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                    catus (Cat)
PubMed=11214318;
M., Douady C., K
                                                                                   Chordata; (Carnivora;
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                                                                                 Craniata; Ver; Fissipedia;
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Mismatches 22;
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N., Springer M.;
two major clades
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ia; Felidae;
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EMBL; AJ251174; CAC16689 1; -.
InterPro; IPM000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1. 1
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"Parallel adaptive
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                                                                                                                                      GEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEEEEEEEEEEECEPQAVP
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IGVFVLCWFPFFFSYSLGAICPKHCKVPHGLF
                                                          ASPASACSPPLQQPQGSRVLATLRGQVLLGRGVGTSSGQWWRRRAQLTREKRFTFVLAVV
                                                                                        VSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFTFVLAVV
                                                                                                                     GAKEEGETPEDPATPALPPSWSALPNSGQGRKEGVCGASPEEEA---
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90.6%;
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Pred. No. 2.9
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SEQUENCE FROM N.A.

Madden O., Willemsen D., Ursing B.M., Arnason U.,
Madden O., Willemsen D., Ursing B.M., Arnason U.,
"Molecular evolution of the alpha 2B adrenergic:
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ dal
EMBL; AJ505820; CAD44321.1; -
EMBL; AJ505820; CAD44321.1; -
EMBL; PF00017; TR000276; GPCR Rhodpsn.
R Pfam; PF00001; 7tm 1; 1.

R PRINTS; PR00237; GPCRRHODDESN.
R PRINTS; PR00237; GPCRRHODDESN.
R PROSITE; PS00237; GPCRRHODDESN.
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01-OCT-2002
01-OCT-2002
01-MAR-2003
                                                                                                                                                                                                                                                                   Manis tetradactyla (Long-tailed pangolin)
Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Pholidota; Manidae; M
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Query Match
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                                                                   Huchon D., Madsen O., Sibbald M.J.J.B., Ament K., Stanhope M., Catzeflis F., de Jong W.W., Douzery E.J.P.,

"Rodent phylogeny and a timescale for the evolution of Glires:
evidence from an extensive taxon sampling using three nuclear:
Mol. Biol. Evol. 0:0-0(2002).

EMBL; AJ427270; CAD20308.1; -

EMBL; AJ427270; CAD20308.1; -

PITRO10276; GPCR_Rhodpsn.

Pfam; PF00001; Tut 1; 1.

PR.NTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; GPCREIN_RECEP_F1_1; 1.

PROSITE; PS00237; GPROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                  01-OCT 2002 (TrEMBLrel. 22, 01-OCT 2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23, Alpha 2B adrenergic receptor
                               Receptor.
NON_TER
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SEQUENCE
                                                                                                                                                                                                                           Erethizon dorgatum (North American porcupine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Erethizontidae;
                                                                                                                                                                                                                                                                                                                     Q8K1U9
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                                                                                                                                                                                                      NCBI_TaxID=34844;
                                                                                                                                                                                                                     Erethizon
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Pred. No. 6.3e.
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01-OCT-2002
01-OCT-2002
01-MAR-2003
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Huchon D., Madsen O., Sibbald M.J.J.B., Ament K., Stanhope M., Catzeflis F., de Jong W.W., Douzery E.J.P.;

"Rodent phylogeny and a timescale for the evolution of Glires: evidence from an extensive taxon sampling using three nuclear: (evidence from an extensive taxon sampling using three nuclear: Mol. Biol. Evol. 0:0-0(2002).

Mol. Biol. Evol. 0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Castor canadensis (Beaver).
Eukaryota; Metazoa; Chordat
Mammalia; Eutheria; Rodenti
NCBI_TaxID=51338;
[1]
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InterPro, IPR000277; GPCR Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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Pred. No. 3.3e-138;
0; Mismatches 26; I
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Q9GL19;
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01-MAR-2001
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Receptor; Trans
NON_TER 1 1
NON_TER 390 390
SEQUENCE 390 AA; 42428 MW; C99055D3EC6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-21082081; PubMed-11214318; Madsen O., Scally M., Douady C., Kac Amrine H., Stanhope M., de Jong W., "Parallel adaptive radiations in two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cynocephalus variegatus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Dermoptera; Cynocephalidae; Cyno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000276; GPCR_Rhodpsn. Pfam; PF00001; 7tm 1; 1. PRINTS; PR00237; GFCRRHODOPSN.
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                                                                                                                                                                                LLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVSRALEYNSKRTFRRIKCII
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(TremBLrel. 16, Last sequence update)
(TremBLrel. 23, Last annotation update)
ergic receptor 2B (Fragment).
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Pred. No. 6.1e-138;
9; Mismatches 26;
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Best Local S
Matches 357
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PROSITE; PS00237; GPCKRHODOPSN.

PROSITE; PS00237; GPROTEIN RECEP F1 1;

PROSITE; PS00262; GPROTEIN RECEP F1 2;

G-protein coupled receptor; Receptor; Tr

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SEQUENCE 395 AA; 43427 MW; 2663DA564
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SEQUENCE FROM N.A.

MEDLINE=21082081; PubMed=11214318;

MEDLINE=21082081; PubMed=11214318;

Madsen O., Scally M., Douady C., Kao D., DeBry

Amrine H., Stanhope M., de Jong W., Springer M.

Amrine H., Stanhope M., de Jong W. appinger M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; AJ251185; CAC16694.1; -.
Interpro; IPR000276; GPCR Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
Pfam; PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation updat
Alpha adrenergic receptor 2B (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9GL12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 409:610-614(2001).
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                            GEKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEEEEEEEEEEEEE----CEPQ
                                                                                                         RIYLIAKRSHRRGPRAKWGPREGESKQPCWVPGG--ASATLPTLASLAASGEANGHSKPI
                                                                                                                                  RIYLIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALASVASAREVNGHSKST
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89.9%;
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Pred. No. 1.7e-137;
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Alpha 2B adrenergic receptor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Madsen O., Willemsen D., Ursing B.M., Arnason U., de Jong W.W.;

Madsen O., Willemsen of the alpha 2B adrenergic receptor.";

"Molecular evolution of the alpha 2B adrenergic receptor.";

Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ505821; CAD44322.1;

EMBL; AJ505811; CAD44322.1;

InterPro; IPR000276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm_1; 1.

PROSITE; PRO0237; GPCRRHODDPSN.

PROSITE; PS00237; G PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Bukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
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NON_TER
SEQUENCE
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VIGVEVLCWEPFEFSYSLGAICPKHCKVPHGLF 405
                                                                                                     PVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFTFVLAV 372
                                                                                                                                                                                                              393
393 AA;
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Search completed: February

6, 2004, 18:19:24

Job time : 33.8896 secs